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OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 272 Seconds  
(without alignments)  
14613.151 Million cell updates/sec

Title:	US-09-601-267-1
Perfect score:	1765
Sequence:	1 agctactcagagcctgaga.....gatatacccccaagctt 1765

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

```
Searched:      2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : N\_Geneseq\_101002.\*

1:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1980 .DAT.*
2:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1981 .DAT.*
3:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1982 .DAT.*
4:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1983 .DAT.*
5:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1984 .DAT.*
6:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1985 .DAT.*
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9:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1988 .DAT.*
10:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1989 .DAT.*
11:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1990 .DAT.*
12:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1991 .DAT.*
13:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1992 .DAT.*
14:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1993 .DAT.*
15:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA1994 .DAT.*
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22:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA2001A .DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA2001B .DAT.*
24:	/SIDS2/gcgdata/geneseq/geneseqn -emb1/NA2002 .DAT.*

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1765	100.0	1765	20	AAt07247	Human telomerase R
2	1719.6	97.4	2426	19	AAV22994	DNA containing hum
3	1640.8	93.0	2425	17	AAT10283	Gene for RNA compo
4	1640.8	93.0	2425	17	AAT11027	DNA encoding the h
5	967.4	54.8	981	19	AAV41194	PstI fragment cont
6	967.4	54.8	981	19	AAV19481	Human telomerase b
7	965.4	54.8	981	24	AAD24234	Human telomerase (
8	965.8	54.7	981	18	AAT82422	Human telomerase c
9	965.8	54.7	981	19	AAV63644	Human telomerase R

[illegible]

## ALIGNMENTS

```

RESULT 1
AAZ07247
ID      AAZ07247 standard; DNA; 1765 BP

```

AAZ07247;

22-OCT-1999 (first entry)

Human telomerase RNA (hTR) gene sequence

Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR; gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

**Homo sapiens**

W09938964-A2.

05-AUG-1999

29-JAN-1999; 99WO-GB00308

29-JAN-1998; 98GB-0001902

(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

Keith WN;

WPI; 1999-479183/40.

Mouse and human telomerase RNA gene promoters, useful for tumor specific gene therapy

Amphipoda

is useful for tumor

PS Disclosure: Fig 1: 109pp: English.

XX  
CC The invention relates to promoter regions from mouse and human telomerase  
CC RNA (TR) component genes. The TR gene promoter can be linked to a  
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy  
CC of cancer, especially neoplasias. The telomerase is necessary for the  
CC unrestricted proliferative capacity of many human cancers. Mutation or  
CC or upregulation of the telomerase repression pathway may cause reactivation  
CC identified in the methods, can be used to block transcription from the TR  
CC gene promoter through interaction of the 5' regulatory sequences. These  
CC substances, e.g. antisense oligonucleotides, transcription factors, the  
CC peptide nucleic acids and factors that disrupt signal transduction, are  
CC useful for cancer therapy. In particular, gene therapy vectors  
CC (especially p67-codapp) comprising the promoter and a viral thymidine  
CC kinase gene can be used to convert a product, e.g. gancyclovir, so that  
CC telomerase RNA gene through manipulation of transcription factors of  
CC effective anticancer therapy and the cloning of the htr gene promoter  
CC allows the analysis of therapeutic molecules which modulate htr promoter  
CC activity. The present sequence represents a human TR (htr) gene sequence.  
XX  
SO Sequence 1765 BP: 404 A; 458 C; 480 G; 423 T; 0 other:

## Query Match

Best Local Similarity 100.0%; Score 1765; DB 20; Length 1765;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTACTCAGAGGCTGAGACGAGAAATCGTTGAACCCGGAGGAGAGTTGCATG 60  
DB 1 AGTACTCAGAGGCTGAGACGAGAAATCGTTGAACCCGGAGGAGAGTTGCATG 60  
QY 61 AGCCGAGATCACCGCATAGACTCCATCCAGCTGGGGAAGAGCAAGACTCCGTCA 120  
DB 61 AGCCGAGATCACCGCATAGACTCCATCCAGCTGGGGAAGAGCAAGACTCCGTCA 120  
QY 121 AAAAAAATGTTTCAATTTATGTTGATTTACCTCTTTTACCTCAATCAACA 180  
DB 121 AAAAAAATGTTTCAATTTATGTTGATTTACCTCTTTTACCTCAATCAACA 180  
QY 181 CAGCACTACTTTAAGCAAGTCAATGATGAAGCGCTTTCTTCTTAATAAGGAG 240  
DB 181 CAGCACTACTTTAAGCAAGTCAATGATGAAGCGCTTTCTTCTTAATAAGGAG 240  
QY 241 ATTGATCTTAAAGTAAATATGATGATGATGATGATGATGATGATGATGATG 300  
DB 241 ATTGATCTTAAAGTAAATATGATGATGATGATGATGATGATGATGATGATG 300  
QY 301 AGGAAAGCTGAGAGGATTTAAGGAAAGGAGGAGGTTGGAATCGGAGCATC 360  
DB 301 AGGAAAGCTGAGAGGATTTAAGGAAAGGAGGAGGTTGGAATCGGAGCATC 360  
QY 361 CCACTGAGCGAGCAAGATTTGCTGATGATGATGATGATGATGATGATGATG 420  
DB 361 CCACTGAGCGAGCAAGATTTGCTGATGATGATGATGATGATGATGATGATG 420  
QY 421 AGTTTCCAAAAATGTGATGATCAAAACTAGGAATTTGTTCTGTTCTTAAAG 480  
DB 421 AGTTTCCAAAAATGTGATGATCAAAACTAGGAATTTGTTCTGTTCTTAAAG 480  
QY 481 AATCTTCCGGAATTTCAATTTTAAAGTATGAGTGAAGCGGCTGCTGAGGCTTA 540  
DB 481 AATCTTCCGGAATTTCAATTTTAAAGTATGAGTGAAGCGGCTGCTGAGGCTTA 540  
QY 541 GGAATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTGGAG 600  
DB 541 GGAATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTGGAG 600  
QY 601 TAAAGAGCAAAAGCTTTCCGGAAGTGGAGAGGCAAGCTCTTCTGATGCGGGA 660  
DB 601 TAAAGAGCAAAAGCTTTCCGGAAGTGGAGAGGCAAGCTCTTCTGATGCGGGA 660  
QY 661 ATGGAATTTTATTTCCGTTCCCGCAACGCGCGCGAGAGAGTACTCTCAGAG 720

DB 661 ATGGAATTTTATTTCCGTTCCCGCAACGCGCGCGAGAGAGTACTCTCAGAG 720  
QY 721 ACCCGGAGAGTCACTTGGCAATCCGTGGGCTGGGCGGCGCTCTTATTAAGCGA 780  
DB 721 ACCCGGAGAGTCACTTGGCAATCCGTGGGCTGGGCGGCGCTCTTATTAAGCGA 780  
QY 781 CTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
DB 781 CTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
QY 841 TGTCTAACCTTAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
DB 841 TGTCTAACCTTAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
QY 901 TCTGCTGATTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
DB 901 TCTGCTGATTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
QY 961 GAGCAAAACAAAAATGTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
DB 961 GAGCAAAACAAAAATGTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
QY 1021 CCGCTGCCAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
DB 1021 CCGCTGCCAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
QY 1081 GCAACCTACTGCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
DB 1081 GCAACCTACTGCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
QY 1141 CGAGGTTGAGGCTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
DB 1141 CGAGGTTGAGGCTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
QY 1201 GATTCCTGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
DB 1201 GATTCCTGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
QY 1261 TGTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
DB 1261 TGTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
QY 1321 GTGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
DB 1321 GTGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
QY 1381 GCACTTCCAAAGTGGGCAAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
DB 1381 GCACTTCCAAAGTGGGCAAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
QY 1441 TGGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
DB 1441 TGGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
QY 1501 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560  
DB 1501 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560  
QY 1561 CCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620  
DB 1561 CCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620  
QY 1621 ATATTTAATTAAGATCTAATTAAGATCTAATTAAGATCTAATTAAGATCTAAT 1680  
DB 1621 ATATTTAATTAAGATCTAATTAAGATCTAATTAAGATCTAATTAAGATCTAAT 1680  
QY 1681 TTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740  
DB 1681 TTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740  
QY 1741 AGTAGATATTAACCCCAAGGCTT 1765

DB	1741	AGTAGATATTAACCCGCCAAGCTT	1765
RESULT	2		
ID	AAV22994		
AC	AAV22994	standard; DNA: 2426 BP.	
XX			
XX	AAV22994:		
DT	30-JUL-1998	(first entry)	
XX			
DE	DNA containing human telomerase RNA component gene sequences.		
XX			
KW	Human: telomerase RNA component gene sequence;		
KW	ribonucleoprotein enzyme; cancer cell; telomerase activity;		
KW	reporter construct; transcription regulatory region;		
KW	prophylaxis; therapy; telomerase-related condition;		
XX	chromatin position effect; ss.		
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	TATA_signal	1438..1444	
FT		/*tag- a	
FT	misc_feature	1238..1259	
FT		/*tag- b	
FT	misc_feature	/note= "PSE consensus sequence"	
FT		1406..1414	
FT		/*tag- c	
FT		/note= "PSE consensus sequence"	
FT	CAT_signal	1399..1406	
FT		/*tag- d	
FT	misc_feature	1354..1359	
FT		/*tag- e	
FT	misc_feature	/note= "SP1 consensus sequence"	
FT		1234..1245	
FT		/*tag- f	
FT		/note= "beta-interferon response element"	
PN	W09811207-A2.		
XX			
PD	19-MAR-1998.		
XX			
PF	16-SEP-1997;	97WO-US16450.	
XX			
PR	16-SEP-1996;	96US-0714482.	
PA	(GERO-) GERON CORP.		
XX			
PI	Harley C, Villeponteau B;		
XX			
DR	WPI: 1998-207376/18.		
XX			
PT	Human telomerase reporter constructs - useful in assays for		
XX	regulators of mammalian telomerase expression		
PS	Claim 6; Pages 27-28; 59pp; English.		
XX			
CC	The present sequence contains human telomerase RNA component gene		
CC	sequences. Telomerase is a ribonucleoprotein enzyme that synthesises		
CC	one strand of the telomeric DNA using as a template a sequence contained		
CC	within the RNA component of the enzyme. Most cancer cells express high		
CC	levels of telomerase activity, while in normal somatic human cells,		
CC	telomerase is not detected. The specification describes the production		
CC	of a telomerase reporter construct which comprises a recombinant		
CC	polynucleotide having a transcription regulatory region of a telomerase		
CC	gene operably linked to a nucleotide sequence encoding a reporter		
CC	polynucleotide heterologous to the transcription regulatory region.		
CC	Expression of the reporter polynucleotide is detectable. The telomerase		
CC	reporter construct is used in screening assays for determining modulator		
CC	of transcription. The modulators can be used for prophylaxis or therapy		
CC	of telomerase-related conditions. The reporter construct which has a		
CC	selectable drug marker can be used to generate position effect reporter		

[illegible]

OS	Homo sapiens.
XX	W09601835-AT-
PD	25-JUN-1991
XX	
PF	06-JUL-1995; 95WO-US08530.
PR	07-JUN-1995; 95US-0482115.
PR	07-JUL-1994; 94US-0272102.
PR	27-OCT-1994; 94US-0330123.
PR	07-JUN-1995; 95US-0472802.
PA	(GERO-) GERON CORP.
PI	Andrews WH, Feng J, Funk W, Villeponteau B;
DR	WPI; 1996-097581/10.
PX	
PT	RNA component of mammalian telomerase, esp. human - useful in
PS	identifying e.g. candidate telomerase-modulating agents
CC	Claim 14; Pages 97-98; 114pp; English.
CC	The present sequence is the gene for the RNA component of human
CC	telomerase (RCHT), which was derived from a genomic DNA library
CC	obt'd. from the human lung fibroblast cell line WI-38. The gene
CC	and the RCHT can be used in the recombinant prodn. of an active
CC	telomerase mol., capable of adding sequences to chromosomal DNA
CC	detection of mutant mammalian telomerase RNA component
CC	polynucleotides. The RCHT may also be used in the identification
CC	of telomerase modulating agents, and in the detection of
CC	telomerase related, or neoplastic conditions in a patient.
CC	Polynucleotides of at least 25 consecutive nucleotides identical,
CC	or complementary to the RCHT sequence linked to heterologous
CC	transcriptional regulatory sequences, can be used for the gene
CC	therapy of human diseases.
SQ	Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;
Query Match	93.0%; Score 1640.8; DB 17; Length 2425;
Best Local Similarity	98.4%; Pred. No. 0;
Matches 1742; Conservative	0; Mismatches 17; Indels 11; Gaps
OY	1 AGCTACTCAGGAGCGTGAGAACAAGAAATCCCTTGACACC CGGAGGAGGTGCATG 60
DB	662 AGCTACTCAGGAGCGTGAGAACAAGAAATCCCTTGAAACCCGGGA-GCAAGGTTCCAGTG 720
OY	61 AGCGGATCACGCCCATGTAGCTTCATCCAGCTGGGCGAAGAGCAAGACATCCGCTTCA 120
DB	721 AGCGGATCACGCCCATGTAGCTTCATCCAGCTGGGCGAAGAGCAAGACATCCGCTTCA 780
OY	121 AAAAAAAAAATGTTACATTTATGTTGATTACTGCCCTCTTTTTTACCTCATCAAGACA 180
DB	781 AAAAAAAAAATGTTACATTTATGTTGATTACTGCCCTCTTTTTTACCTCATCAAGACA 840
OY	181 CAGCACTACTTTAAAGCAAAGTCATGATTTGAAGAGCCCTTCTTCATAATTAAGGAG 240
DB	841 CAGCACTACTTTAAAGCAAAGTCATGATTTGAAGAGCCCTTCTTCATAATTAAGGAG 900
OY	241 ATTGAGTCTTAAATTAATTAATGATTAGTTACCTTGATTTAAAGCCATCCTGCTCA 300
DB	901 ATTGAGTCTTAAATTAATTAATGATTAGTTACCTTGATTTAAAGCCATCCTGCTCA 960
OY	301 AGGAACTCTGGAGAGGCAATTTAAAGAAAAAGGGCGAGGTTGGAATCTGGAACGCATC 360
DB	961 AGGAACTCTGGAGAGGCAATTTAAAGAAAAAGGGCGAGGTTGGAATCTGGAACGCATC 1020
OY	361 CCAGTAGCCGAGACAAAGATCTCTGTAGTACATGCTGCTGGGAATGATTTTCAAA 420
DB	1021 CCAGTAGCCGAGACAAAGATCTCTGTAGTACATGCTGCTGGGAATGATTTTCAAA 480

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Oy 421 AGTTCTCAAAAAATGTGATCAAAACTAGSAATTAAGTGTCTGTGCTTAGGCCCTA 480
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Db 1081 AGTTCTCAAAAAATGTGATCAAAACTAGSAATTAAGTGTCTGTGCTTAGGCCCTA 1140
Oy 481 AATCTTCTGTGAATTCATTTTAAAGTAGTCGAGGTGAACCGCTGTGCTGTCAGA 540
    |||||||
Db 1141 AATCTTCTGTGAATTCATTTTAAAGTAGTCGAGGTGAACCGCTGTGCTGTCAGA 1200
Oy 541 GGTAGAAAAAGCGCTGTGATACCTCAAGTAGTTTACCTTTAAAGAGTCCGAAG 600
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Db 1201 GGTAGAAAAAGCGCTGTGATACCTCAAGTAGTTTACCTTTAAAGAGTCCGAAG 1260
Oy 601 TAAAGACGAAGACCTTTCCGAGCTGGGGAAGGCAACGTCCTTCATGAGCGGAA 660
    |||||||
Db 1261 TAAAGACGAAGACCTTTCCGAGCTGGGGAAGGCAACGTCCTTCATGAGCGGAA 1320
Oy 661 ATGGAACCTTAAATTCCTCCCTCCCAACCAAGCCCGCGAGAGTAGTCTCAAGAG 720
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Db 1321 ATGGAACCTTAAATTCCTCCCTCCCAACCAAGCCCGCGAGAGTAGTCTCAAGAG 1380
Oy 721 AGCGGGAAGTAGCTGTGGCCAAATCCGTGGGTGGCGCGCTCCCTTATAAGCCGA 780
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Db 1381 AGCGGGAAGTAGCTGTGGCCAAATCCGTGGGTGGCGCGCTCCCTTATAAGCCGA 1440
Oy 781 CTGCGCCGCGACGCGACCGGGTTTC---GAGGGTGGGCTGGAGGGGTGGGCAAT 836
    |||||||
Db 1441 CTGCGCCGCGACGCGACCGGGTTGGGGAAGGAGGTGGGCTGGAGGGGTGGGCAAT 1500
Oy 837 TTTTCTCTAACCTTAAGTAGAGAGGCGTAGGCGCTTCTTCTCCCGCGCGCTG 896
    |||||||
Db 1501 TTTTCTCTAACCTTAAGTAGAGAGGCGTAGGCGCTTCTTCTCCCGCGCGCTG 1560
Oy 897 TTTTCTCTGCTGCTTTCAGCGCGGGGAAAAAGCTGGGCTGGCGCTTCCACCTTCAT 956
    |||||||
Db 1561 TTTTCTCTGCTGCTTTCAGCGCGGGGAAAAAGCTGGGCTGGCGCTTCCACCTTCAT 1620
Oy 957 TCTAGAGCAAAACAAAATGTCAAGTCTGTGCGCCGCTCCCGCGGGGACCTCGCG 1016
    |||||||
Db 1621 TCTAGAGCAAAACAAAATGTCAAGTCTGTGCGCCGCTCCCGCGGGGACCTCGCG 1679
Oy 1017 GGGTGGCTGGCCAGCGCCCGGAACCCCGCTGGAGGCGCGCGGTCTCTCC 1076
    |||||||
Db 1680 GGGTGGCTGGCCAGCGCCCGGAACCCCGCTGGAGGCGCGCGGTCTCTCC 1137
Oy 1077 GGAGGACCTTACGTGGCAGCGCGGAAGATT-GGCTGTGTAGCGCGGGGTCTCGGGGGG 1135
    |||||||
Db 1738 GGAGGACCTTACGTGGCAGCGCGGAAGATTGGGCTGTGTAGCGCGGGGTCTCGGGGGG 1197
Oy 1136 GAGGCGGAGGTTTCAGGCTTTAGCGCGGAGAGAGAGAGGAGGAGTCCCGCGCGC 1195
    |||||||
Db 1798 GAGGCGGAGGTTTCA-CCGTTTCAAGGCGCGAGAGAGAGAGGAGGAGT-CCCGCGCGC 1855
Oy 1196 GGGCGGATTCCTGTGAGCTGTGGAGCTGCACCCAGAGCTCGGCTCAACATGACATTGCG 1255
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Db 1856 GGGCGGATTCCTGTGAGCTGTGGAGCTGCACCCAGAGCTCGGCTCAACATGACATTGCG 1915
Oy 1256 TTTTCTGTGGTGGGGGGAAGCGGATTCGTGGCATTCCGCAACCTTCCCGCGCAATTGG 1315
    |||||||
Db 1916 TTTTCTGTGGTGGGGGGAAGCGGATTCGTGGCATTCCGCAACCTTCCCGCGCAATTGG 1975
Oy 1316 GGGTGTGAAACCCCAAACTGTACTGTGGGCACTGTGTCAAAATTGGCAGAGAGC 1375
    |||||||
Db 1976 GGGTGTGAAACCCCAAACTGTACTGTGGGCACTGTGTCAAAATTGGCAGAGAGC 2035
Oy 1376 TGAAGGACCTTCAAAAGTGGGCAAAATGAGTGGAGGAGTGAAGCGGGGTTTCCCTGAGCC 1435
    |||||||
Db 2036 TGAAGGACCTTCAAAAGTGGGCAAAATGAGTGGAGGAGTGAAGCGGGGTTTCCCTGAGCC 2095
Oy 1436 GTTTCCTGGTGGGTTTCCCGCTTCTCCGCTTTTGTGCTTTTAAAGTGTATTAACAAC 1495
    |||||||
Db 2096 GTTTCCTGGTGGGTTTCCCGCTTCTCCGCTTTTGTGCTTTTAAAGTGTATTAACAAC 2155

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Oy 1496 TTAGTCTGCTCTGTCAGATTGTTGAGGTTTTGCTTCTCCCAAGTAGATCTGACC 1555
    |||||||
Db 2156 TTAGTCTGCTCTGTCAGATTGTTGAGGTTTTGCTTCTCCCAAGTAGATCTGACC 2215
Oy 1556 AGTCCCTCAACGGGCTGTGGGAAACAGTCATTTTTTTTGAAGATCATTTTAACATT 1615
    |||||||
Db 2216 AGTCCCTCAACGGGCTGTGGGAAACAGTCATTTTTTTTGAAGATCATTTTAACATT 2275
Oy 1616 AATGAATTTTAAATTAAGAGATTAATGAACATTCGAATGTGTTCCTTAAATGTCA 1675
    |||||||
Db 2276 AATGAATTTTAAATTAAGAGATTAATGAACATTCGAATGTGTTCCTTAAATGTCA 2335
Oy 1676 TCGGTTTATGCCAGAGATTAGAATTCTTTTGAATAATTAGACCTTGGCGATGACCT 1735
    |||||||
Db 2336 TCGGTTTATGCCAGAGATTAGAATTCTTTTGAATAATTAGACCTTGGCGATGACCT 2395
Oy 1736 TGAAGATGAGATATTAACCCCAAGCTT 1765
    |||||||
Db 2396 TGAAGATGAGATATTAACCCCAAGCTT 2425

RESULT 4
AAT11027
ID AAT11027 standard; DNA; 2425 BP.
XX
AC AAT11027;
XX
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the human telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
KW plasmid; probe; primer; ribozyme; ss.
XX
OS Homo sapiens.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US08620.
XX
PR 07-JUN-1995; 95US-0485778-
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 13-FEB-1995; 95US-0387524.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AH, Feng J, Funk W, Greider C;
PI Maruenda MA, Villeponteau B;
XX
DR WPI: 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in
PT studying cell senescence and immortalisation
XX
PS Claim 37; Figure 1; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially
CC from mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the
CC telomerase; probes and primers can be used in detection; vectors and
CC host cells transformed with the isolated telomerase genes can be
CC used for production of telomerases; RNA and DNA ribozymes and triplex
CC forming oligonucleotides directed against the telomerase genes can
CC be used therapeutically as can plasmids. A mouse which lacks the
CC telomerase gene (also claimed) can be used for study of telomere
CC regulation in vivo, and the role it plays in immortalisation. This
CC DNA sequence encodes the human telomerase RNA component.
XX
Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;

```

Query Match 93.0%: Score 1640.8; DB 17; Length 2425;  
 Best Local Similarity 98.4%: Pred. No. 0;  
 Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8;

1 AGCTACTGAGAGGCTGAGACAGAGATCCGTTGAACCCGGAGGAGAGAGTGCAGTG 60  
 Db AGCTACTGAGAGGCTGAGACAGAGATCCGTTGAACCCGGAGGAGAGTGCAGTG 720  
 Oy AGCGAGATCGCGGCTAGACTCCATCCAGCTGGGCGAAGAGCAAGACTCCGTCTCA 120  
 Db AGCGAGATCGCGGCTAGACTCCATCCAGCTGGGCGAAGAGCAAGACTCCGTCTCA 780  
 Oy 121 AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTTTTTCCTTAATAAAGAG 180  
 Db AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTTTTTCCTTAATAAAGAG 840  
 Oy 181 CAGACTACTTTAAAGCAAGTCAATGTAAGAGCGCTTCTTCTTAATAAAGAGAG 240  
 Db CAGACTACTTTAAAGCAAGTCAATGTAAGAGCGCTTCTTCTTAATAAAGAGAG 900  
 Oy 241 ATTGAGTCTTAAGATTAATATGATAGTTACATTTGATTAAGCCATCTCTGCTCA 300  
 Db ATTGAGTCTTAAGATTAATATGATAGTTACATTTGATTAAGCCATCTCTGCTCA 960  
 Oy 301 AGGAGAGCTGAGAGAGGCAATTTAAAGAAAGGGGCGAGGTTGAAGCTCGAGCGATC 360  
 Db AGGAGAGCTGAGAGAGGCAATTTAAAGAAAGGGGCGAGGTTGAAGCTCGAGCGATC 1020  
 Oy 361 CCAGTGGCGGAGACAGATTCGTCTGATCAGTGTGCTGGGAATCTAATTTTACAA 420  
 Db CCAGTGGCGGAGACAGATTCGTCTGATCAGTGTGCTGGGAATCTAATTTTACAA 1080  
 Oy 421 ACTTCTCCAAAAATGATGATCAAAACTAGGAATTAAGTCTGCTGCTTGGGCGCTA 480  
 Db ACTTCTCCAAAAATGATGATCAAAACTAGGAATTAAGTCTGCTGCTTGGGCGCTA 1140  
 Oy 481 AATTTTCTCTGATTTCCATTTTAAAGTATGAGTGAAGCGGCTGTGCTGCTCAGA 540  
 Db AATTTTCTCTGATTTCCATTTTAAAGTATGAGTGAAGCGGCTGTGCTGCTCAGA 1200  
 Oy 541 GGATAGAAAAAGGCGCTGATACCTCAAGTAACTTCACTTTAAAGAGGTCGGAG 600  
 Db GGATAGAAAAAGGCGCTGATACCTCAAGTAACTTCACTTTAAAGAGGTCGGAG 1260  
 Oy 601 TAAAGACGCAAGCCCTTCCGAGCTGCGGAAGGCAAGCTCTTCTCATGCGCGAA 660  
 Db TAAAGACGCAAGCCCTTCCGAGCTGCGGAAGGCAAGCTCTTCTCATGCGCGAA 1320  
 Oy 661 ATGGAATTTAATTTCCGTTCCCGTCCCAACAGCCCGCGAGAGTACTCTCAGAG 720  
 Db ATGGAATTTAATTTCCGTTCCCGTCCCGTCCCAACAGCCCGCGAGAGTACTCTCAGAG 1380  
 Oy 721 AGCCGAGAGTCAAGCTTCCGATCCGTTGCGGCGGCGCTCCCTTTAAAGCGCA 780  
 Db AGCCGAGAGTCAAGCTTCCGATCCGTTGCGGCGGCGCTCCCTTTAAAGCGCA 1440  
 Oy 781 CTCGCGCGGCGAGCGACCGGGTTTC---GAGAGGTGGGCTGAGAGGGGTGGTGGCAT 836  
 Db CTCGCGCGGCGAGCGACCGGGTTTC---GAGAGGTGGGCTGAGAGGGGTGGTGGCAT 1500  
 Oy 837 TTTTGTCTTAACCTTAAGTGAAGGGGTAGGCGCGCTTTTGTCTCCCGCGCGCTG 896  
 Db TTTTGTCTTAACCTTAAGTGAAGGGGTAGGCGCGCGCTTTTGTCTCCCGCGCGCTG 1560  
 Oy 897 TTTTCTGCTGACTTTTCAAGCGGGGGAAGAAAGCTTCGCGCTCCGCTTCAACCTTCA 956  
 Db TTTTCTGCTGACTTTTCAAGCGGGGGAAGAAAGCTTCGCGCTCCGCTTCAACCTTCA 1620  
 Oy 957 TCTAGAGCAAAACAAATATGTCAGTGTGGCGCTTGGCCCTTCGCGGAGCTGCGGC 1016  
 Db TCTAGAGCAAAACAAATATGTCAGTGTGGCGCTTGGCCCTTCGCGGAGCTGCGGC 1679

Oy 1017 GGGTGGCTTCCAGAGCCCGGAAACCCCGCTGAGAGCGGGGCTGGGCGGCTTCTCC 1076  
 Db GGGTGGCTTCCAGAGCCCGGAAACCCCGCTGAGAGCGGGGCTGGGCGGCTTCTCC 1737  
 Oy 1077 GAGAGCACTACTGCGACCGCGGAAGATT--GGCTCTGTACAGCCGCGGTCTCTGGGGGC 1135  
 Db GAGAGCACTACTGCGACCGCGGAAGATT--GGCTCTGTGTAGCCGCGGTCTCTGGGGGC 1797  
 Oy 1136 GAGGGCAGGTTTCAAGGCTTTTCAAGCCGCGAGAGAGGAAGGAGGAGTCCCGGCGGC 1195  
 Db GAGGGCAGGTTTCAAGGCTTTTCAAGCCGCGAGAGAGGAAGGAGGAGTCCCGGCGGC 1855  
 Oy 1196 GGGCGATTTCCCTGACCTGTGGAGCTGCAACCGAGACTCGGCTCAGATGCTTCCG 1255  
 Db GGGCGATTTCCCTGACCTGTGGAGCTGCAACCGAGACTCGGCTCAGATGCTTCCG 1915  
 Oy 1256 TTTTCTGTTGGTGGGGGAAGCGGATTCGTTGGGCAATCCGCTCACCCCTCGCGAGTGGG 1315  
 Db TTTTCTGTTGGTGGGGGAAGCGGATTCGTTGGGCAATCCGCTCACCCCTCGCGAGTGGG 1975  
 Oy 1316 GGGTGTGAACCCCAACCTGACTGAGGCGAGTGTGCTGCAAAATTGGCAGAGAGC 1375  
 Db GGGTGTGAACCCCAACCTGACTGAGGCGAGTGTGCTGCAAAATTGGCAGAGAGC 2035  
 Oy 1376 TGAAGGCACTTCCAAAGTGGGCAAAATGAATGGCAGTGAAGCGGGGTTGCTGGAGCC 1435  
 Db TGAAGGCACTTCCAAAGTGGGCAAAATGAATGGCAGTGAAGCGGGGTTGCTGGAGCC 2095  
 Oy 1436 GTTCCGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTTATGTTGATTAACAG 1495  
 Db GTTCCGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTTATGTTGATTAACAG 2155  
 Oy 1496 TTAGTCTCTGCTGTGAGATTTTGTGAGTGTGCTTCCCAAGGTAGTCTGAGC 1555  
 Db TTAGTCTCTGCTGTGAGATTTTGTGAGTGTGCTTCCCAAGGTAGTCTGAGC 2215  
 Oy 1556 AGTCCCTCAAGCGGGTGTGGAGAAAGTCAATTTTGTGAGAGATTAATTAACATT 1615  
 Db AGTCCCTCAAGCGGGTGTGGAGAAAGTCAATTTTGTGAGAGATTAATTAACATT 2275  
 Oy 1616 AATGAATTTTATTAAGAGATCTAATGAACATTGGAATGTGCTTAAATGTGCA 1675  
 Db AATGAATTTTATTAAGAGATCTAATGAACATTGGAATGTGCTTAAATGTGCA 2335  
 Oy 1676 TCGGTTTATGCGAGAGGTTTGAAGTCTTTTGAAGAAATTAACCTTGGCGATGACT 1735  
 Db TCGGTTTATGCGAGAGGTTTGAAGTCTTTTGAAGAAATTAACCTTGGCGATGACT 2395  
 Oy 1736 TGAGCAGTAGATATTAACCCCAAGCTT 1765  
 Db TGAGCAGTAGATATTAACCCCAAGCTT 2425

RESULT 5  
 AAV41194 standard; DNA; 981 BP.  
 AAV41194:  
 08-OCT-1998 (first entry)  
 PstI fragment containing RNA component of human telomerase (hTR).  
 RNA component: human telomerase; antisense oligonucleotide; infection;  
 neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
 contraception; sterilisation; immunosuppression; therapeutic; hTR;  
 immune system down-regulation; anti-inflammatory therapy; ss.  
 Homo sapiens.  
 OS  
 XX  
 XX  
 FH  
 FT  
 misc\_feature 266..716  
 /tag- a

FT	misc_feature	/note= "RNA component of human telomerase (hTR)"
FT	311...320	
FT	/tag= b	
FT	/note= "template region of hTR"	
XX	MO9828442-A1.	
XX	02-JUL-1998.	
XX	19-DEC-1997;	97WO-US23619.
XX	20-DEC-1996;	96US-0770565.
XX	20-DEC-1996;	96US-0770564.
XX	(GERO-) GERON CORP.	
XX	Kealey JT, Kim NW, Pruzan R, Weinlich SL, Wu F:	
XX	WPI: 1998-377670/32.	
XX	Disclosure: Page 53; 80pp; English.	
XX	This represents a PstI fragment containing the RNA component of human	
XX	telomerase (hTR). The invention provides antisense oligonucleotides	
XX	(AAV41169 to AAV41181) to hTR. These antisense oligonucleotides	
XX	specifically hybridize to a nucleotide sequence within an accessible	
XX	region of the hTR, but that does not hybridize to a sequence within the	
XX	template region of hTR. These oligonucleotides may specifically be used	
XX	for detection of an RNA component of human telomerase in a sample. This	
XX	is useful for diagnosing cancer (especially neuroblastoma, bladder, colon	
XX	and prostate cancer), and providing prognosis for a cancer patient. The	
XX	inhibitory oligonucleotides can inhibit the telomerase activity level in	
XX	a cell by interfering with transcription of the RNA component, decreasing	
XX	assembly of the RNA component into the telomerase holoenzyme, or	
XX	inhibiting the polymerase activity of telomerase. These antisense	
XX	oligonucleotides can be used for inhibiting telomerase activity in both	
XX	cultured cells and in cells in vivo. They can be used in therapeutics for	
XX	treating or preventing cancer, for contraception or sterilisation, for	
XX	immunosuppression, and for selectively down-regulating specific branches	
XX	of the immune system, e.g. a specific subset of T-cells, in anti-	
XX	inflammatory therapies or for treating infections by, e.g. yeast,	
XX	parasites or fungi.	
XX	Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;	
XX	Query Match	54.8%; Score 967.4; DB 19; Length 981;
XX	Best Local Similarity	99.8%; Pred. No. 1.3e-261;
XX	Matches	979; Conservative 0; Mismatches 1; Indels 1; Gaps 1
QY	534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG	593
DB	1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG	60
QY	594 TCGGAAGTAAAGACCAAAAGCCTTTCGCCGAGCTGCGGAAGGCAACGTCCTTCATG	653
DB	61 TCGGAAGTAAAGACCAAAAGCCTTTCGCCGAGCTGCGGAAGGCAACGTCCTTCATG	120
QY	654 GCCGGAATGGAACCTTAAATTCGCCGTTCCGCCCAACGAGCCGCCGAGAGATGATC	713
DB	121 GCCGGAATGGAACCTTAAATTCGCCGTTCCGCCCAACGAGCCGCCGAGAGATGATC	180
QY	714 TCACAGAGACCCGAGAGATCAGCTTGGCCAAATCCGTCGCTGGGCGCGCTCCCTTAT	773
DB	181 TCACAGAGACCCGAGAGATCAGCTTGGCCAAATCCGTCGCTGGGCGCGCTCCCTTAT	240
QY	774 AAGCCGACTGCGCCGGCAGCCGACCGGGGTGGGAGGAGGTGGGCTGGAGGGGTGGTGC	833
DB	241 AAGCCGACTGCGCCGGCAGCCGACCGGGGTGGGAGGAGGTGGGCTGGAGGGGTGGTGC	300

Oy	834	CATTTTTGTCTAACCCCTAACTAGAGAAGGCGTAGCGGCCGTTCCTTTCCTCCCGCGC	893
Db	301	CATTTTTTGTTCTAACCCTTAAC TAGAAGGGCGTAGGCGCCGTTCCTTTCCTCCCGCGC	360
Oy	894	CTGTTTTTCTCGCGACTTTCAGCGGGCGGAAGAAGCTCGGGCTCGCGCTTCGCACGCTT	953
Db	361	CTGTTTTTCTCGCGACTTTCAGCGGGCGGAAGAAGCTCGGGCTCGCGCTTCGCACGCTT	420
Oy	954	CATTCTAGAGCAAAACAATAATGTCTAGCTGTGGCCCGCTTCGCCCTCCCGGGACCTGC	1013
Db	421	CATTCTAGAGCAAAACAATAATGTCTAGCTGTGGCCCGCTTCGCCCTCCCGGGACCTGC	480
Oy	1014	GCGGGGTTCGCTCGCCACGCCCCCGGAACCCCCTCTGGAAGCCCGCGGTGGCGGGGGCTTC	1073
Db	481	GCGGGGTTCGCTCGCCACGCCCCCGGAACCCCCTCTGGAAGCCCGCGGTGGCGGGGGCTTC	540
Oy	1074	TCCGAGAGCACACTCTACTSCACCGCGAAGAAGTT--GGCTCTGTACGCGCGGCGTCTTCGCG	1132
Db	541	TCCGAGAGCACACCCTCTCCACCGCGAAGAAGTTGGCTCTGTACGCGCGGCGTCTTCGCG	600
Oy	1133	GCGGAGGGCGAGTTCAGGCTTCAGGCTTCAGGCGCGAGAGAAGACGAGAGTCCCGCG	1192
Db	601	GCGGAGGGCGAGTTCAGGCTTCAGGCTTCAGGCGCGAGAGAAGACGAGAGTCCCGCG	660
Oy	1193	GCGGGCGCGANTCCCTCTAGCTGTGGGACGTCACCCAGACCTCGGCTTCACACATCATTT	1252
Db	661	GCGGGCGCGANTCCCTCTAGCTGTGGGACGTCACCCAGACCTCGGCTTCACACATCATTT	720
Oy	1253	CGCTTTCCTGTGGTGGGGGGAACGCCGATCGGCGCATCGCTCAACCCCTCGCGCGAGT	1312
Db	721	CGCTTTCCTGTGGTGGGGGGAACGCCGATCGGCGCATCGCTCAACCCCTCGCGCGAGT	780
Oy	1313	GGGGGCTTGTGAACCCCAACCTGACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGGAG	1372
Db	781	GGGGGCTTGTGAACCCCAACCTGACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGGAG	840
Oy	1373	ACGTGAAGGACCACTCCCAAACTCGGCGCAAAAATGAAATGGGACGAGACCGGGGTTCCTCGA	1432
Db	841	ACGTGAAGGACCACTCCCAAACTCGGCGCAAAAATGAAATGGGACGAGACCGGGGTTCCTCGA	900
Oy	1433	GCCGTTTCCTCGGAGGCTTCGCCGCTTCGCCCTTTTGTTCGCTTTAATGATTGATTATC	1492
Db	901	GCCGTTTCCTCGGAGGCTTCGCCGCTTCGCCCTTTTGTTCGCTTTAATGATTGATTATC	960
Oy	1493	AAC TTAGTTCCTGCTGCAG 1513	
Db	961	AAC TTAGTTCCTGCTGCAG 981	
RESULT 6			
AAVL19481			
ID	AAVL19481	standard; cDNA; 981 BP.	
XX	AAVL19481:		
XX	28-AUG-1998	(first entry)	
DT	Human telomerase hTR gene.		
XX	Human telomerase hTR gene.		
DE	Telomerase; hTR gene; TPC2; TPC3; telomere length; human; cancer;		
KW	gene therapy; diagnosis; ss.		
KX	Homo sapiens.		
OS			
XX	Key	Location/Qualifiers	
FH	FT unsure	21	
FT	mRNA	/+tag= a	
FT		266..715	
FT		/+tag= b	
NN	WO9811204 -A1.		

PD 19-MAR-1998.  
XX  
PF 13-SEP-1996; 96WO-US14679.  
XX  
PR 13-SEP-1996; 96WO-US14679.  
XX  
PA (GERO-) GERON CORP.  
XX  
PI Adams RR, Andrews WH, Feng J, Villeponteau B;  
XX  
DR WPI: 1998-207373/18.  
XX  
PT Human TPC2, TPC3 and TR genes - regulate telomere length or modulate  
PI telomerase activity  
XX  
PS Disclosure: Fig 9A-B; 86pp; English.  
XX  
CC This nucleotide sequence comprises an approximately 1 kb PstI  
CC restriction fragment of plasmid pGRN33 that includes the human  
CC telomerase hTR gene. hTR3 mRNA levels correlate with telomerase  
CC activity levels in a variety of mortal and immortal cell lines.  
CC In methods of the invention, measurements of telomere length,  
CC telomerase activity or hTR levels can be used to identify immortal  
CC cells, such as cancer cells, and to evaluate the proliferative  
CC capacity of the cell. Gene therapy vectors encode useful nucleic  
CC acids such as hTR, or antisense nucleic acids or ribozymes that  
CC target TPC2, TPC3 (see AAV19479-80) and/or hTR gene products.  
XX  
XX Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other:

Query Match 54.88; Score 967.4; DB 19; Length 981;  
Best Local Similarity 99.88; Pred. No. 1.3e-261;  
Matches 979; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
DB 1  
534 CTGAGAGATAGAAAAAGCCCTGTGATACCTGATAGTTTACCTTTAAAGAG 593  
1 CTGAGAGATAGAAAAAGCCCTGTGATACCTGATAGTTTACCTTTAAAGAG 60  
594 TCGGAAGTAAAGCGCAACGCTTTCCGAGCGTGGGAAAGGCGCAACGTCCTTCTCATG 653  
61 TCGGAAGTAAAGCGCAACGCTTTCCGAGCGTGGGAAAGGCGCAACGTCCTTCTCATG 120  
654 GCGGGAAGTGAATTTATTTCCGTTCCCGCAACGCGCGCGGAGAGAGTACTC 713  
121 GCGGGAAGTGAATTTATTTCCGTTCCCGCAACGCGCGCGGAGAGAGTACTC 180  
714 TCAAGAGAGCGGAGAGTACCTTGGCCAAATCGTGGCGGCGCTCCCTTTAT 773  
181 TCAAGAGAGCGGAGAGTACCTTGGCCAAATCGTGGCGGCGCTCCCTTTAT 240  
774 AAGCCGACTCGCCGCGAGCGACCGGTTGGGAGGCGGCGCTGGAGGGGTGTGGC 833  
241 AAGCCGACTCGCCGCGAGCGACCGGTTGGGAGGCGGCGCTGGAGGGGTGTGGC 300  
834 CATTTTGTCTAACCTTACTGAGAGGGCGTAGGCGCGCTGTTTGTCTCCCGCG 893  
301 CATTTTGTCTAACCTTACTGAGAGGGCGTAGGCGCGCTGTTTGTCTCCCGCG 360  
894 CTGTTTCTCGCTGACTTTCAGCGGGGAGAAAGCTTCGCGCTCCGCTTCCACGCTT 953  
361 CTGTTTCTCGCTGACTTTCAGCGGGGAGAAAGCTTCGCGCTCCGCTTCCACGCTT 420  
954 CATTTAGAGCAAAATAATGTACGTGCTGCGCGCTTCGCGCGGAGACCTGC 1013  
421 CATTTAGAGCAAAATAATGTACGTGCTGCGCGCTTCGCGCGGAGACCTGC 480  
1014 GCGGGTGGCTTC 1073  
481 GCGGGTGGCTTC 540  
1074 TCCGAGGACACTTACTGCGACCGGAGAGATT-GGCTGTGACCGCGGCTCTCTGGG 1132  
541 TCCGAGGACACTTACTGCGACCGGAGAGATTGGGCTCTGTGACCGCGGCTCTGGG 600

QY 1133 GCGGAGGCGAGTTCAGGCTTTACGCGCCGAGAGAGCAAGGAGGAGTCCCGCG 1192  
DB 601 GCGGAGGCGAGTTCAGGCTTTACGCGCCGAGAGAGCAAGGAGGAGTCCCGCG 660  
QY 1193 GCGGCGCGATTCCTGAGCTGTGGACGTGACCGCAGAGCTCGCTACACATGAGTT 1252  
DB 661 GCGGCGCGATTCCTGAGCTGTGGACGTGACCGCAGAGCTCGCTACACATGAGTT 720  
QY 1253 CGCTTCTCTGTGTGGGAGAAAGCGGATGTGCGCATCCGTACCCCTCGCGGAGT 1312  
DB 721 CGCTTCTCTGTGTGGGAGAAAGCGGATGTGCGCATCCGTACCCCTCGCGGAGT 780  
QY 1313 GCGGCGCTGTGAGACCCCAAACTGATGAGGCGGATGTGCGCATCCGTACCCCTCGCGGAGT 1372  
DB 781 GCGGCGCTGTGAGACCCCAAACTGATGAGGCGGATGTGCGCATCCGTACCCCTCGCGGAGT 840  
QY 1373 ACCTGAAAGCAGCTCCAAAGTGGGCCAAATGATGAGGAGAGGAGGAGTGGCTGGA 1432  
DB 841 ACCTGAAAGCAGCTCCAAAGTGGGCCAAATGATGAGGAGAGGAGGAGTGGCTGGA 900  
QY 1433 GCGGCTCTGCGGCGGCTTCCGCTTCCGCTTTTGTGCTTTATGCTTATATAC 1492  
DB 901 GCGGCTCTGCGGCGGCTTCCGCTTCCGCTTTTGTGCTTTATGCTTATATAC 960  
QY 1493 AACTTAGTCTCTGCTGTGAG 1513  
DB 961 AACTTAGTCTCTGCTGTGAG 981

RESULT 7  
AAND24234  
ID AAND24234 standard; DNA: 981 BP.

AC AAND24234;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Human telomerase (hTR) gene.  
XX  
KW Human; telomerase; TR; telomerase activity-related disease; therapy;  
XX cancer; pregnancy; fertility; ds.  
XX  
OS Homo sapiens.  
XX  
FH  
FT Key Location/Qualifiers  
FT misc\_feature 267..715  
FT /\*tag= "a  
FT /note= "hTR transcript serves as template in the  
FT telomerase ribonucleoprotein"

US6300110-B1.  
XX  
PD 09-OCT-2001.  
XX  
PF 23-DEC-1998; 98US-0220157.  
XX  
PR 09-SEP-1995; 95US-003492P.  
PR 13-SEP-1996; 96US-0710249.  
PR 05-JUN-1996; 96US-0583808.  
XX  
PA (GERO-) GERON CORP.  
XX  
PI Villeponteau B, Feng J, Andrews WH, Adams RR;  
XX  
DR WPI: 2002-033174/04.  
XX

Peptide products of the human TPC2 and TPC3 gene are involved in  
regulation of telomere length and activity are useful to diagnose and  
treat telomere length and activity-related diseases -  
Example: Fig 9; 60pp; English.



CC The invention relates to methods and reagents for regulating telomere  
CC length and for modulating telomerase activity in mammalian cells. The  
CC invention also relates to purified, synthetic or recombinant peptides  
CC such as TPC2 or TPC3 used for detecting regulators of telomere length  
CC and telomerase activity in mammalian cells and for a variety of related  
CC diagnostic and therapeutic purposes. The method is useful for screening,  
CC diagnosing, monitoring and treating diseases and other conditions such as  
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.  
CC The present sequence is human telomerase (hTR) gene.  
XX

Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.8%; Score 966.4; DB 24; Length 981;  
Best Local Similarity 99.7%; Pred. No. 2.5e-261;  
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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OY 534 CTGCAGAGATGAAAAAGGCCCTCTGATPACCTCAAGTTACTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATPACCTCAAGTTACTTTACCTTTAAAGAGG 60
OY 594 TCGGAAGTAAAGACCGCAAGCCCTTCCGAGGTGGGAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACCGCAAGCCCTTCCGAGGTGGGAAGGCAACGTCCTTCATG 120
OY 654 GCCGGAATGGAACCTTATTTCCCGTTCCCCCAACAGCCGCCCGGAGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTATTTCCCGTTCCCCCAACAGCCGCCCGGAGAGAGTACTC 180
OY 714 TCACGAGACCCCGAGAGTACAGCTTGGCCAATCCGTGCGGTGGCGGCGCTCCCTTAT 773
DB 181 TCACGAGACCCCGAGAGTACAGCTTGGCCAATCCGTGCGGTGGCGGCGCTCCCTTAT 240
OY 774 AAGCGACTGCGCCGCGACGACCGGTTGGGAGAGGTGGGCTGGAGGGGTGTGGC 833
DB 241 AAGCGACTGCGCCGCGACGACCGGTTGGGAGAGGTGGGCTGGAGGGGTGTGGC 300
OY 834 CATTTTGTCTAACCTTACTAGAGAGGCGTAGCGCGCTTCTCTCCCGCGG 893
DB 301 CATTTTGTCTAACCTTACTAGAGAGGCGTAGCGCGCTTCTCTCCCGCGG 360
OY 894 CTTGTTTTCCTGCTGACTTTCAGCGGGGGAAGGCTTGGCGCTTCCACCGTT 953
DB 361 CTTGTTTTCCTGCTGACTTTCAGCGGGGGAAGGCTTGGCGCTTCCACCGTT 420
OY 954 CATTTAGAGCAAAATAATGTGAGTGTGGCCGCTTCCCGCCCTCCCGGGAGCTGC 1013
DB 421 CATTTAGAGCAAAATAATGTGAGTGTGGCCGCTTCCCGCCCTCCCGGGAGCTGC 480
OY 1014 GCGGGGTGCGCTGCGCAGCCCGGAAACCCGCTGAGGCGCGGTGGCGCGGGCTTC 1073
DB 481 GCGGGGTGCGCTGCGCAGCCCGGAAACCCGCTGAGGCGCGGTGGCGCGGGCTTC 540
OY 1074 TCCGGAAGGCACTACTGCCACCGCGAAGATT- GCGTCTGTCAAGCCGGGCTCTCGGG 1132
DB 541 TCCGGAAGGCACTACTGCCACCGCGAAGATTGCGCTGTGTAGCGCGGGTCTCTCGGG 600
OY 1133 GCGGAAGGGGAGGTTCAAGGCTTTTCAGGCGGCAAGAGGAAGGAGGAGTCCCGGG 1192
DB 601 GCGGAAGGGGAGGTTCAAGGCTTTTCAGGCGGCAAGAGGAAGGAGGAGTCCCGGG 660
OY 1193 GCGGGCGCATTCCTCTGAGCTGTGGACGTGCACCCAGAGTCTGCTCAGATGCAATT 1252
DB 661 GCGGGCGCATTCCTCTGAGCTGTGGACGTGCACCCAGAGTCTGCTCAGATGCAATT 720
OY 1253 CGCTTTCCTGTGTGTGGGGGAACCGCGATCGTGGCCATTCGTCACCCCTCGCGGCACT 1312
DB 721 CGCTTTCCTGTGTGTGGGGGAACCGCGATCGTGGCCATTCGTCACCCCTCGCGGCACT 780
OY 1313 GGGGGCTTGTGAACCCCAAAACCTGACTGACGTGGCCAGTGTGCTCAAAATTGGCAGAG 1372
DB 781 GGGGGCTTGTGAACCCCAAAACCTGACTGACGTGGCCAGTGTGCTCAAAATTGGCAGAG 840
OY 1373 AGGTGAAGCACCTCCCAAAAGTGGCCAAATGATGGCAGTGAAGCGGGGTTGCCGTGA 1432

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DB 841 ACCTGAAGCACCTCCAAAGTCGGCCAAATGATGAGCAGTGAAGCGGGGTTGCCGTGA 900
OY 1433 GCCGTTCTCGCTGGGTGTCTCCGTTCTCCGTTTGTGCTTTATAGTTGATTTAC 1492
DB 901 GCCGTTCTCGCTGGGTGTCTCCGTTCTCCGTTTGTGCTTTATAGTTGATTTAC 960
OY 1493 AACTTGTCTCGCTGTGCAG 1513
DB 961 AACTTGTCTCGCTGTGCAG 981

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RESULT 8
AAT89242
ID AAT89242 standard; DNA; 981 BP.
XX
AC AAT89242;
XX
DT 12-MAY-1998 (first entry)
XX
DE Clone containing hTR sequence.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; human telomerase RNA; hTR; ds.
XX
OS Synthetic.
XX
FH Homo sapiens.
XX
FT Key Location/Qualifiers
FT misc_difference 265..716
FT FT /*tag= a
FT FT /*note= "human telomerase RNA"
XX
PN W09738013-A1.
XX
PD 16-OCT-1997.
XX
PF 09-APR-1997; 97MO-US05931.
XX
PR 09-APR-1996; 96US-0630019.
XX
PA (GERO-) GERON CORP.
XX
PI Corey D, Norton JC, Platyszek MA, Shay JW, Wright WE;
XX
DR WPI: 1997-512647/47.
XX
PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT used to inhibit telomerase, for treating tumours and other
PT proliferative diseases, also for diagnosis
XX
PS Disclosure: Pages 20-21; 76pp; English.
XX
CC This fragment of cloned DNA contains the human telomerase RNA (hTR)
CC sequence, (266-716bp). The hTR region contains a CCC template which
CC the peptide nucleic acid (PNA) can recognise. The presence of a GGG
CC in the PNAs allows for the specific hybridisation to the template
CC region of this hTR component. PNAs can be used as probes to detect the
CC RNA component of mammalian telomerase and as inhibitors of telomerase
CC activity, especially in the treatment of cancer.
XX
SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

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Query Match 54.7%; Score 965.8; DB 18; Length 981;  
Best Local Similarity 99.7%; Pred. No. 3.6e-261;  
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

OY 534 CTGCAGAGATGAAAAAGGCCCTCTGATPACCTCAAGTTACTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATPACCTCAAGTTACTTTACCTTTAAAGAGG 60
OY 594 TCGGAAGTAAAGACCGCAAGCCCTTCCGAGGTGGGAAGGCAACGTCCTTCATG 653
DB 1 TCGGAAGTAAAGACCGCAAGCCCTTCCGAGGTGGGAAGGCAACGTCCTTCATG 653

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Db      61  TCGAAGTAAGACGCAAGCCTTCCCGAGCTGCGGAGGCAAGCTCCTCTCATG 120
Oy      654  GCCGGAATGGAACCTTATTTCCCGTTCCCGCCACACGCGCGGAGAGTACTC 713
Db      121  GCCGGAATGGAACCTTATTTCCCGTTCCCGCCACACGCGCGGAGAGTACTC 180
Oy      714  TCACAGAGCGCGAGACTGAGTGGCCAAATCCGTGGGTGGGCGGCGCTTAT 773
Db      181  TCACAGAGCGCGAGACTGAGTGGCCAAATCCGTGGGTGGGCGGCGCTTAT 240
Oy      774  AAGCGGATCCCGCGACGCGGCTGCGAGGGTGGGCTGGAGGGGTGTGTC 833
Db      241  AAGCGGATCCCGCGACGCGGCTGCGAGGGTGGGCTGGAGGGGTGTGTC 300
Oy      834  CATTTTGTCTAACCCCTAACTAGAGAGGGGTAGGGCGCGCTGCTTTGCTCCCGCG 893
Db      301  CATTTTGTCTAACCCCTAACTAGAGAGGGGTAGGGCGCGCTGCTTTGCTCCCGCG 360
Oy      894  CTGTTTTCTGCGACTTTTCAGCGGGCGGAAAGCCTGCGCGCTTCCACCGTT 953
Db      361  CTGTTTTCTGCGACTTTTCAGCGGGCGGAAAGCCTGCGCGCTTCCACCGTT 420
Oy      954  CATTTAGAGCAACAAATAATGTCAGTGTGCGCGCTTCCCGCGGAGCTGC 1013
Db      421  CATTTAGAGCAACAAATAATGTCAGTGTGCGCGCTTCCCGCGGAGCTGC 480
Oy      1014  GCGGGTCCGCTGCCACGCGCCGCAACCCGCGCTGAGAGCGCGGTGGCGCGGGGCTTC 1073
Db      481  GCGGGTCCGCTGCCACGCGCCGCAACCCGCGCTGAGAGCGCGGTGGCGCGGGGCTTC 540
Oy      1074  TCGGAGGCAACCTACTCTCCACCGGAGAGTT- GCGTCTGTCAGCGCGGGTCTTCGGG 1132
Db      541  TCGGAGGCAACCTACTCTCCACCGGAGAGTTGCGGTCTGTCAGCGCGGGTCTTCGGG 600
Oy      1133  GCGGAGGCGAGGTTTCAGGCTTTTCAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1192
Db      601  GCGGAGGCGAGGTTTCAGGCTTTTCAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 660
Oy      1193  GCGGAGGCGAGTTCCCTGAGCTGTGGAGCTGACCCAGAGAGAGAGAGAGAGAGAGAG 1252
Db      661  GCGGAGGCGAGTTCCCTGAGCTGTGGAGCTGACCCAGAGAGAGAGAGAGAGAGAGAG 720
Oy      1253  CGCTTCTCTGTTGGTGGGAGAGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 1312
Db      721  CGCTTCTCTGTTGGTGGGAGAGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 780
Oy      1313  GGGGGCTTGTGAACCCCAAACTGACTGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 1372
Db      781  GGGGGCTTGTGAACCCCAAACTGACTGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 840
Oy      1373  ACGTGAAGCAGCTCCAAAGTGGGCGCAAAATGAGTGGCGGAGTGGCGGAGTGGCGGAG 1432
Db      841  ACGTGAAGCAGCTCCAAAGTGGGCGCAAAATGAGTGGCGGAGTGGCGGAGTGGCGGAG 900
Oy      1433  GCGGTCCTGCGTGGTCTCCGCTTCCGCTTTTGTGCTTTAGGTTGATATAC 1492
Db      901  GCGGTCCTGCGTGGTCTCCGCTTCCGCTTTTGTGCTTTTATGTTGATATAC 960
Oy      1493  AACTTAGTCTGCTGTGAG 1513
Db      961  AACTTAGTCTGCTGTGAG 981

```

RESULT 9  
AAV63644  
ID AAV63644 standard; DNA: 981 BP.

AAV63644;

15-FEB-1999 (first entry)

Human telomerase RNA component sequence from lambda clone 28-1.

```

KW      Lambda clone 28-1; human; telomerase RNA component; anticancer therapy;
KM      assay; vaccine; cancer; purification; ss.
XX
OS      Synthetic.
OS      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      misc_feature
FT      266..716
FT      /tag= a
FT      /note= "human telomerase RNA component sequence"
XX
PN      WO9845450-A1.
PD      15-OCT-1998.
XX
PD      04-APR-1997; 97WO-US06012.
XX
PD      04-APR-1997; 97WO-US06012.
XX
PR      (GERO-) GERON CORP.
XX
PI      Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA.
PI      Vasserot AP, Weinrich SL;
XX
DR      WPI: 1998-594485/50.
XX
PT      Purification of telomerase on affinity material - useful for, e.g.
PT      diagnosis and treatment of cancer
XX
PS      Disclosure: Pages 14-15; 76pp: English.
XX
CC      The present sequence represents the PstI fragment of the 2.4 kb
CC      Sautiral-HindIII fragment of lambda clone 28-1. This clone contains
CC      human telomerase RNA component gene sequences. The specification
CC      provides methods for purifying human telomerase. The methods involve
CC      the use of several sequential steps, including the use of two matrices
CC      that bind molecules bearing negative charges, a matrix that binds
CC      molecules bearing positive charges, an affinity purification step
CC      and a size separation. Telomerase is a particular target of anticancer
CC      therapies, and is useful in assays for characterizing (pre)cancerous
CC      cells. The present sequence can be used for such assays. Telomerase can
CC      also be used to screen for specific modulators, for biochemical analysis
CC      of its activity, and in preparation of antibodies. Fragments of
CC      telomerase, or nucleic acid encoding them, are used in vaccines, and
CC      for treating over expression of telomerase, particularly in cancer.
XX
SQ      Sequence 981 BP: 172 A; 303 C; 305 G; 200 T; 1 other;

```

Query Match 54.7%; Score 965.8; DB 19; Length 981;  
Best Local Similarity 99.7%; Pred. No. 3.6e-261;  
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Oy      534  CTGCAAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593
Db      1  CTGCAAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
Oy      594  TCGAAGTAAAGACGCAAGCCTTCCCGGAGCGTGGCGAAGGGAAGAGTCTCTCATG 653
Db      61  TCGAAGTAAAGACGCAAGCCTTCCCGGAGCGTGGCGAAGGGAAGAGTCTCTCATG 120
Oy      654  GCGGAAATGGAACCTTAATTTCCCGTTCCCGCCAAACACGCGCGCGGAGAGTACTC 713
Db      121  GCGGAAATGGAACCTTAATTTCCCGTTCCCGCCAAACACGCGCGCGGAGAGTACTC 180
Oy      714  TCACAGAGCGCGGAGAGTCAAGTGGCCAAATCCGTGGGTGGGCGGCTTAT 773
Db      181  TCACAGAGCGCGGAGAGTCAAGTGGCCAAATCCGTGGGTGGGCGGCTTAT 240
Oy      774  AAGCGGATCCCGCGACGCGGCTGCGAGGGTGGGCTGGAGGGGTGTGTC 833
Db      241  AAGCGGATCCCGCGACGCGGCTGCGAGGGTGGGCTGGAGGGGTGTGTC 300
Oy      834  CATTTTGTCTAACCCCTAACTAGAGAGGGGTAGGGCGCGCTTTCCTCCCGCGG 893

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|||||
Db 301 CATTTTGTCTAACTAGAGAGGCGTAGGCGGCTTTGTGCTCCCGCGG 360
Oy 894 CTGTTTTCTCGTGACTTTACAGCGGGGAAAAGCTGGCGCTTCCACCGTT 953
Db 361 CTGTTTTCTCGTGACTTTACAGCGGGGAAAAGCTGGCGCTTCCACCGTT 420
Oy 954 CATTTAGAGCAAAACAAAATGTACGTGCTGGCCCTTCCCGGGAGACTGC 1013
Db 421 CATTCAGAGCAAAACAAAATGTACGTGCTGGCCCTTCCCGGGAGACTGC 480
Oy 1014 GCGGGTCCCTCCAGCGAGCGCGGAAACCCCGCTGAGGCGCGGCTTCC 1073
Db 481 GCGGGTCCCTCCAGCGAGCGCGGAAACCCCGCTGAGGCGCGGCTTCC 540
Oy 1074 TCCGGAGGACCTACAGCCAGCGCGGAAAGATT-GGCTGTGTACGCCG 1132
Db 541 TCCGGAGGACCTACAGCCAGCGCGGAAAGATTGTGTACGCCGCGGCT 600
Oy 1133 GCGAGGCGGAGGTTTCAGGCTTTTCAGCGCGGAGAAAGAGAGAGTCC 1192
Db 601 GCGAGGCGGAGGTTTCAGGCTTTTCAGCGCGGAGAAAGAGAGAGTCC 660
Oy 1193 CCGGCGCGATTCCTGAGCTGTGGAGCTGCACCCAGAGCTCGCTCAAC 1252
Db 661 CCGGCGCGATTCCTGAGCTGTGGAGCTGCACCCAGAGCTCGCTCAAC 720
Oy 1253 CGCTTTCCTGTGGTGGGGGGAAGCGCGATCGTGGCGATTCGTCACCC 1312
Db 721 CGCTTTCCTGTGGTGGGGGGAAGCGCGATCGTGGCGATTCGTCACCC 780
Oy 1313 GGGGCGTTGTGAACCCCAACCTGACTGACTGAGCGGAGTGTCTCAATT 1372
Db 781 GGGGCGTTGTGAACCCCAACCTGACTGACTGAGCGGAGTGTCTCAATT 840
Oy 1373 ACCTGAGGACCTTCCAAAGTGGGCAAAATGAGTGGGAGTGGCGGTT 1432
Db 841 ACCTGAGGACCTTCCAAAGTGGGCAAAATGAGTGGGAGTGGCGGTT 900
Oy 1433 GCGGTCCTGCGGCGGTTTCCCGCTTCCCGCTTTTGTGTTTGTGTTAC 1492
Db 901 GCGGTCCTGCGGCGGTTTCCCGCTTCCCGCTTTTGTGTTTGTGTTAT 960
Oy 1493 AACTTAGTTCGTGCTGCTGAG 1513
Db 961 AACTTAGTTCGTGCTGCTGAG 981

RESULT 10
AA233626
ID AA233626 standard: DNA; 981 BP.
XX
AC AA233626:
XX
DT 07-JAN-2000 (first entry)
XX
DE Human clone 28-1 containing telomerase fragment.
XX
KM Telomerase: human; Immune response: cancer; vaccine: treatment;
KW disease: ss.
XX
OS Homo sapiens.
XX
PN US968506-A.
XX
PD 19-OCT-1999.
XX
PF 04-APR-1997; 97US-0833377.
XX
PR 04-AUG-1995; 95US-0510736.
XX
PA (GERO-) GERON CORP.
XX
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PI Atkinson EM, Lichtsteiner SP, Weinlich SL, Pruzan RA, Kealey JR;
PI Vasserot AP;
XX
XX WPI: 1999-590379/50.
XX
XX Compositions comprising human telomerase, useful for treating diseases
XX associated with overexpression of telomerase e.g. cancer -
XX
XX Disclosure: Column 41-42: 34pp; English.
XX
XX This invention describes a novel composition comprising human telomerase
XX having at least 2000-fold (preferably at least 6000-fold) increased
XX relative purity compared with crude extract of cells from
XX adenovirus-transformed kidney cell line. The composition is useful for
XX eliciting an immune response in animals and may therefore be used as a
XX vaccine for treating diseases associated with the overexpression of
XX telomerase e.g. cancer. This sequence represents a nucleic acid fragment
XX from human clone 28-1 which contains a fragment of the human telomerase
XX described in the method of the invention.

SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 20; Length 981;
Best Local Similarity 99.7%; Pred. No. 3,6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 534 CTGCAGAGATAGAAAAAGCCCTCTGATFACCTCAAGTTAGTTTACCTTTAAAG 593
Db 1 CTGCAGAGATAGAAAAAGCCCTCTGATFACCTCAAGTTAGTTTACCTTTAAAG 60
Oy 594 TCGAGATGAAGACGAAAGCCCTTCCGAGCTGGGAAAGGCAAGTCTCTCATG 653
Db 61 TCGAGATGAAGACGAAAGCCCTTCCGAGCTGGGAAAGGCAAGTCTCTCATG 120
Oy 654 GCGGAAATGGAATTAAATTCCTCCGTTCCCAACAGCCCGCGGAGAGTACTC 713
Db 121 GCGGAAATGGAATTAAATTCCTCCGTTCCCAACAGCCCGCGGAGAGTACTC 180
Oy 714 TCACGAGCCCGGAGAGTACGTTGCCAATCCGTCGCGGCGGCTTCTTAT 773
Db 181 TCACGAGCCCGGAGAGTACGTTGCCAATCCGTCGCGGCGGCTTCTTAT 240
Oy 774 AAGCCGACTCGCCGCGACGCGACCGGTTGGCGAGAGTGGGCTGGAGGGTGGCG 833
Db 241 AAGCCGACTCGCCGCGACGCGAGCGGTTGGCGAGAGTGGGCTGGAGGGTGGCG 300
Oy 834 CATTTTGTCTAACCTTAACCTGAGAAAGGCGTAGGCGCGCTTCTCCCGCGG 893
Db 301 CATTTTGTCTAACCTTAACCTGAGAAAGGCGTAGGCGCGCTTCTCCCGCGG 360
Oy 894 CTGTTTTTCTCGTGACTTTACAGCGGGGCGAAAGCTGGCGCTTCCACCGTT 953
Db 361 CTGTTTTTCTCGTGACTTTACAGCGGGGCGAAAGCTGGCGCTTCCACCGTT 420
Oy 954 CATTTAGAGCAAAACAAAATGTACGTGCTGGCCCTTCCCGGGAGACTGC 1013
Db 421 CATTCAGAGCAAAACAAAATGTACGTGCTGGCCCTTCCCGGGAGACTGC 480
Oy 1014 GCGGGTCCCTCCAGCGAGCGCGGAAACCCCGCTGAGGCGCGGCTTCC 1073
Db 481 GCGGGTCCCTCCAGCGAGCGCGGAAACCCCGCTGAGGCGCGGCTTCC 540
Oy 1074 TCCGGAGGACCTACAGCCAGCGCGGAAAGATT-GGCTGTGTACGCCG 1132
Db 541 TCCGGAGGACCTACAGCCAGCGCGGAAAGATTGTGTACGCCGCGGCT 600
Oy 1133 GCGAGGCGGAGGTTTCAGGCTTTTCAGCGCGGAGAAAGAGAGAGTCC 1192
Db 601 GCGAGGCGGAGGTTTCAGGCTTTTCAGCGCGGAGAAAGAGAGAGTCC 660
Oy 1193 CCGGCGCGATTCCTGAGCTGTGGAGCTGCACCCAGAGCTCGCTCAACATG 1252
Db 661 CCGGCGCGATTCCTGAGCTGTGGAGCTGCACCCAGAGCTCGCTCAACATG 720
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QY 1253 CGCTTCCTGTTGGTGGGGGAAACCCGATCTGCGCATCCGTACACCCCTGCGCGCAGT 1312  
 |||||||  
 Db 721 CGCTTCCTGTTGGTGGGGGAAACCCGATCTGCGCATCCGTACACCCCTGCGCGCAGT 780  
 QY 1313 GGGGCGTTGTAACCCCAACCTGACTAGTGGCCAGTGTGTCGCAATTTGGCAGAG 1372  
 |||||||  
 Db 781 GGGGCGTTGTAACCCCAACCTGACTAGTGGCCAGTGTGTCGCAATTTGGCAGAG 840  
 QY 1373 AGGTGAAGGACCTGCAAAAGTGGCCCAAAATGAATGGCAGTACCGGGGTTGGCTTGA 1432  
 |||||||  
 Db 841 AGGTGAAGGACCTGCAAAAGTGGCCCAAAATGAATGGCAGTACCGGGGTTGGCTTGA 900  
 QY 1433 GCGCTTCCGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTGTTATAC 1492  
 |||||||  
 Db 901 GCGCTTCCGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTGTTATAC 960  
 QY 1493 AACTTAGTTCCCTGCTCTGAC 1513  
 |||||||  
 Db 961 AACTTAGTTCCCTGCTCTGAC 981

## RESULT 11

AAA37564  
 ID AAA37564 standard; DNA; 981 BP.

AC AAA37564;

XX 15-AUG-2000 (first entry)

XX Human telomerase nucleotide sequence.

XX Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 KW Inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 KW paternity testing; ds.

XX Homo sapiens.

XX US6046307-A.

XX 04-APR-2000.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1996; 96US-0630019.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX WPI; 2000-292432/25.

XX New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 PT activity in mammalian cells is useful as probes to detect the RNA  
 XX component of a mammalian telomerase

XX Disclosure: Column 13-14; 45pp; English.

XX The present sequence represents the human telomerase nucleotide sequence.  
 CC The invention relates to peptide nucleic acid molecules which hybridise  
 CC to the mRNA component of mammalian telomerase, and inhibit telomerase  
 CC activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one  
 CC strand of the telomeric DNA, using as a template an 11 nucleotide  
 CC sequence contained within the RNA component of the enzyme. The invention  
 CC relates to PNA molecules having a sequence of no more than 25 bases,  
 CC which include the sequence GTTAGG. The unchanged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency

CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity. In combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on hTR gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component.

SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 21; Length 981;  
 Best Local Similarity 99.7%; Pred. No. 3.6e-261;  
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 534 CTGCGAGAGATGAAGAAAAAGGCGCTCTGTATCCTCAAGTTAGTTCACTTTAAAGAG 593  
 |||||||  
 Db 1 CTGCGAGAGATGAAGAAAAAGGCGCTCTGTATCCTCAAGTTAGTTCACTTTAAAGAG 60  
 QY 594 TCGGAAGTAAAGCAAAAGCCTTCCCGGACGTGCGGAAGGCAAGTCCTCTCATG 653  
 |||||||  
 Db 61 TCGGAAGTAAAGCAAAAGCCTTCCCGGACGTGCGGAAGGCAAGTCCTCTCATG 120  
 QY 654 GCGGGAATGGAACCTTATTTCCGCTCCGCCCAACAGCGCCCGGAGAGAGTACTC 713  
 |||||||  
 Db 121 GCGGGAATGGAACCTTATTTCCGCTCCGCCCAACAGCGCCCGGAGAGAGTACTC 180  
 QY 714 TCACGAGACCGCGGAGACTCAGCTTGGCCAAATCCGTGCGGTGGGCGCCGCTTTAT 773  
 |||||||  
 Db 181 TCACGAGACCGCGGAGACTCAGCTTGGCCAAATCCGTGCGGTGGGCGCCGCTTTAT 240  
 QY 774 AAGCGACTGCGCGCGGACGCGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 833  
 |||||||  
 Db 241 AAGCGACTGCGCGCGGACGCGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 QY 834 CATTTTGTCTAAACCTTAAGTGAAGGCGTAAAGGCGCTTTTGTCTCCCGCGG 893  
 |||||||  
 Db 301 CATTTTGTCTAAACCTTAAGTGAAGGCGTAAAGGCGCTTTTGTCTCCCGCGG 360  
 QY 894 CTGTTTCTGCTGACTTTCAGCGGCGGAGAAAGCCTCGGCTGCGGCTTTCACCGTT 953  
 |||||||  
 Db 361 CTGTTTCTGCTGACTTTCAGCGGCGGAGAAAGCCTCGGCTGCGGCTTTCACCGTT 420  
 QY 954 CATTTGAGCAAAACAAAATGTCAAGCTGCGCGCTTTCGCGGCTTTCGCGGAGCTTC 1013  
 |||||||  
 Db 421 CATTTGAGCAAAACAAAATGTCAAGCTGCGCGCTTTCGCGGCTTTCGCGGAGCTTC 480  
 QY 1014 GCGGAGTGCCTGCGCGGCGCGCGGAGAACCCCGCTGAGAGCGCGGCTGCGGCGGCTTC 1073  
 |||||||  
 Db 481 GCGGAGTGCCTGCGCGGCGCGGAGAACCCCGCTGAGAGCGCGGCTGCGGCGGCTTC 540  
 QY 1074 TCGGAGGACCACTACTGCGACCGCGAAGATT-GGCTGTGTAGCGCGGCTTCGCGG 1132  
 |||||||  
 Db 541 TCGGAGGACCACTACTGCGACCGCGAAGATTGGCTGTGTAGCGCGGCTTCGCGG 600  
 QY 1133 GCGGAGGCGAGGTTCAGGCTTTAGGCGCCGAGGAAGAGAGAGAGAGAGAGAGAGAG 1192  
 |||||||  
 Db 601 GCGGAGGCGAGGTTCAGGCTTTAGGCGCCGAGGAAGAGAGAGAGAGAGAGAGAGAG 660  
 QY 1193 GCGGCGGATTTCCCTGAGCTGTGAGACGTGACCAAGAGAGAGAGAGAGAGAGAGAT 1252  
 |||||||  
 Db 661 GCGGCGGATTTCCCTGAGCTGTGAGACGTGACCAAGAGAGAGAGAGAGAGAGAGAT 720  
 |||||||  
 QY 1253 CGCTTTCCTGTTGGTGGGGGAAACCCGATCTGCGCATCCGTACACCCCTGCGCGCAGT 1312

```

DB 721 CGCTTCTCTGTGGTGGGGGAAGCCGATCGTGGCATCCGTACACCCCTCGCGGAGT 780
      |||
QY 1313 GGGGGCTTGTGAACCCCAAACTGACTGACTGGCCAGTGTGCTGCAATTGGCAGAG 1372
      |||
DB 781 GGGGGCTTGTGAACCCCAAACTGACTGACTGGCCAGTGTGCTGCAATTGGCAGAG 840
      |||
QY 1373 ACGTGAAGCAGCTCCAAAGTCCGCCAAATGAATGGGAGTGAAGCCGGGGTGGCCGTGA 1432
      |||
DB 841 ACGTGAAGCAGCTCCAAAGTCCGCCAAATGAATGGGAGTGAAGCCGGGGTGGCCGTGA 900
      |||
QY 1433 GCGGTCCTGCGTGGGTTCTCCGCTTCGCTTTTGTGCTTTATGTTATATAC 1492
      |||
DB 901 GCGGTCCTGCGTGGGTTCTCCGCTTCGCTTTTGTGCTTTATGTTATATATAC 960
      |||
QY 1493 AACTAGTCTGCTGCGAG 1513
      |||
DB 961 AACTAGTCTGCTGCGAG 981
      |||

RESULT 12
AAS15442
ID AAS15442 standard: DNA: 981 BP.
AC AAS15442:
XX
DT 14-FEB-2002 (first entry)
XX
DE Pct1 fragment containing human telomerase RNA component gene sequence.
XX
KW Mammalian: forensic; paternity testing; human telomerase RNA component;
KW hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease;
KW autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia;
KW HIV; AIDS; human immunodeficiency virus; telomere metabolism; cytoskeletal;
KW acquired immunodeficiency syndrome; anti-inflammatory; immunosuppressive;
KW bacteriophage lambda clone 28-1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 266..716
      /*tag= a
      /note= "htr gene sequence"
      /*tag= b
      /note= "template region of htr used as template for
      synthesis of telomeric repeats"
FT misc_feature 311..320
      /*tag= b
      /note= "template region of htr used as template for
      synthesis of telomeric repeats"
FT
FT
XX
XX US6294650-B1.
XX
XX 25-SEP-2001.
XX
XX 08-JUL-1999: 99US-0349532.
XX
XX 09-APR-1997: 97US-0838545.
XX
XX 09-APR-1996: 96US-0630019.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PA
XX
XX Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC;
XX
XX WPI: 2001-638024/73.
XX
XX
XX New peptide nucleic acids that hybridises to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases -
XX
XX Disclosure: Column 13-16: 46pp; English.
XX
XX
XX The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridising to the RNA component of mammalian
XX
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CC telomerase. The PNAs are useful as probes to detect the RNA component
CC of mammalian telomerase and as inhibitors of telomerase activity, or to
CC detect and/or quantitate polynucleotide having the human telomerase
CC RNA component (hTR) sequence, as well as in forensic identification of
CC individuals, such as paternity testing or identification of criminal
CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC PNA can be further used for treating or preventing cancer, inflammation,
CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC diseases. The PNAs in combination with other pharmaceuticals (such as
CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents a Pct1 fragment, derived
CC from bacteriophage lambda clone 28-1, containing the hTR gene sequence.
XX
SQ Sequence 981 BP: 172 A; 303 C; 305 G; 200 T; 1 other:
XX
Query Match 54.7%; Score 965.8; DB 23; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1:
QY 534 CTGCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTATGTTTCACTTTAAAGAG 593
      |||
DB 1 CTGCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTATGTTTCACTTTAAAGAG 60
      |||
QY 594 TCGGAAGTAAAGACGCAACCTTTCCCGAGCTGCGGAAGGGACAGTCTTCTCATG 653
      |||
DB 61 TCGGAAGTAAAGACGCAACCTTTCCCGAGCTGCGGAAGGGACAGTCTTCTCATG 120
      |||
QY 654 GCGGAAATGGAACCTTAATTTCCCGTCCGCCCAACACAGCCGCCGAGAGATGATC 713
      |||
DB 121 GCGGAAATGGAACCTTAATTTCCCGTCCGCCCAACACAGCCGCCGAGAGATGATC 180
      |||
QY 714 TCACGAGAGCCGCGAGAGTACGCTTGCGCAATCCGTGCGTGGGCGCTCCCTTAT 773
      |||
DB 181 TCACGAGAGCCGCGAGAGTACGCTTGCGCAATCCGTGCGTGGGCGCTCCCTTAT 240
      |||
QY 774 AAGCGACCTGCGCGGAGCGACCGGCTTGCGAGGCTGCGGAGGAGGAGTGGC 833
      |||
DB 241 AAGCGACCTGCGCGGAGCGACCGGCTTGCGAGGCTGCGGAGGAGGAGTGGC 300
      |||
QY 834 CATTTTGTCTAACCTTAATGAGAGGCGTAGGCGCGCTGTTTGTCCCGCGCG 893
      |||
DB 301 CATTTTGTCTAACCTTAATGAGAGGCGTAGGCGCGCTGTTTGTCCCGCGCG 360
      |||
QY 894 CTGTTTTCCTGCTGACTTTCAGCGGGGAAAAAGCCTGCGGCTGCGCTCCACCTT 953
      |||
DB 361 CTGTTTTCCTGCTGACTTTCAGCGGGGAAAAAGCCTGCGGCTGCGCTCCACCTT 420
      |||
QY 954 CATTTAGAGCAAAATATGTCAAGTGTGCGGCTGCGGCTTCCCGGGAGCTGC 1013
      |||
DB 421 CATTTAGAGCAAAATATGTCAAGTGTGCGGCTGCGGCTTCCCGGGAGCTGC 480
      |||
QY 1014 GCGGAGTCTGCTGCCCGCCAGCCCGCAACCCGCTGAGAGCGGCGTGGCGGGGCTTC 1073
      |||
DB 481 GCGGAGTCTGCTGCCCGCCAGCCCGCAACCCGCTGAGAGCGGCGTGGCGGGGCTTC 540
      |||
QY 1074 TCCGAGGACACTACTGCAACCGGAGAGATT--GGCTGTGTCAAGCGGAGTCTTCGGG 1132
      |||
DB 541 TCCGAGGACACTACTGCAACCGGAGAGATTGGGCTGTGTCAAGCGGAGTCTTCGGG 600
      |||
QY 1133 GCGGAGGAGAGTTCAGGCTTTCAGGCGCGAGAGAGAGAGAGAGAGTCCCGCG 1192
      |||
DB 601 GCGGAGGAGAGTTCAGGCTTTCAGGCGCGAGAGAGAGAGAGAGAGTCCCGCG 660
      |||
QY 1193 GCGGAGGAGATTCCTAGAGTGTGAGAGTGCACCCAGAGCTGCGGCTCAACATGCAATT 1252
      |||
DB 661 GCGGAGGAGATTCCTAGAGTGTGAGAGTGCACCCAGAGCTGCGGCTCAACATGCAATT 720
      |||
QY 1253 CGCTTCTCTGTGGTGGGGGAAGCCGATCGTGGCATCCGTACACCCCTCGCGGAGT 1312
      |||
DB 721 CGCTTCTCTGTGGTGGGGGAAGCCGATCGTGGCATCCGTACACCCCTCGCGGAGT 780
      |||
```

[illegible]

QY	534	CTGCAGAGGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCAACCTTTAAAGAG	593
Db	1	CTGCAGAGGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCAACCTTTAAAGAG	60
QY	594	TCCGAGTAAGAAGCGAAGAGCCTTTCCCGAGCTGGCGAAGGGCAACGTCCTTCATG	653
Db	61	TCCGAGTAAGAAGCGAAGAGCCTTTCCCGAGCTGGCGAAGGGCAACGTCCTTCATG	120
QY	654	GCCGGAATGGAACTTTAAATTTCCGTTCCCTCCCAACCGAGCCCGCGAGAGTGACATC	713
Db	121	GCCGGAATGGAACTTTAAATTTCCGTTCCCTCCCAACCGAGCCCGCGAGAGTGACATC	180
QY	714	TCCAGGAGACCCGGGAGAGTCAGCTTGCGCAATCCGTCGCGTGGCGCGCCGCTCCCTTAT	773
Db	181	TCCAGGAGACCCGGGAGAGTCAGCTTGCGCAATCCGTCGCGTGGCGCGCCGCTCCCTTAT	240
QY	774	AAGCCGACATCGCCCGGACCGGAGTGGGAGGGTGGGGCCCTGGAGAGGGTGTGGC	833
Db	241	AAGCCGACATCGCCCGGACCGGAGTGGGAGGGTGGGGCCCTGGAGAGGGTGTGGC	300
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Db	301	CATTTTGTCTTAACCTTAAGAGAGGCGCTAGGCGCGCTTTTGTCTTCCCGCGCG	360
QY	894	CGTTTTCCTCCCTACCTTTTACGGGGGGGGAAGACCTTCGGCTTCGCGCTTCACCGTT	953
Db	361	CGTTTTCCTCCCTACCTTTTACGGGGGGGGAAGACCTTCGGCTTCGCGCTTCACCGTT	420
QY	954	CATTCTAAGCAAAACAAAAATGTCAGCTGCTGGCGCTTGGCCCTCCGGGGACCTGC	1013
Db	421	CATTCTAAGCAAAACAAAAATGTCAGCTGCTGGCGCTTGGCCCTCCGGGGACCTGC	479
QY	1014	GCGGGTGCCTGCCACACCCCGAAGCCCGCTTGGAGGCGCGGTCGCGCGGGGCTTC	1073
Db	480	GCGGGTGCCTGCCACACCCCGAAGCCCGCTTGGAGGCGCGGTCGCGCGGGGCTTC	539
QY	1074	TCCGAGGACACTACTGCGACCGCGAAGAGTT-GGCTCTGACACCGCGGGTCTCTGGG	1132
Db	540	TCCGAGGACACTACTGCGACCGCGAAGAGTTGGGCTCTGACACCGCGGGTCTCTGGG	599
QY	1133	GCGCAGGGCGAGGTTTCAGGCTTTCAAGCCGCGAGAAAGAGAAAGGAGAGTCCCGCG	1192
Db	600	GCGCAGGGCGAGGTTTCAGGCTTTCAAGCCGCGAGAAAGAGAAAGGAGAGTCCCGCG	659
QY	1193	GCGCGGCGAGTTCCCTAGGCTGGGGAGCTGGACCCAGAGACTGGGCTACACATGCAATT	1252
Db	660	GCGCGGCGAGTTCCCTAGGCTGGGGAGCTGGACCCAGAGACTGGGCTACACATGCAATT	719
QY	1253	CGCTTTCCTTGGTGGGGGAACGCGGATCGATGCGCATCCGTCACACCTCCGCGGACAGT	1312
Db	720	CGCTTTCCTTGGTGGGGGAACGCGGATCGATGCGCATCCGTCACACCTCCGCGGACAGT	779
QY	1313	GGGGGCTTGTGAACCCCAACCTGACTGACTGGGCACTGTCCTCAAAATTGGCAGAG	1372
Db	780	GGGGGCTTGTGAACCCCAACCTGACTGACTGGGCACTGTCCTCAAAATTGGCAGAG	839

QY 1373 ACGTGAAGCACCCTCCAAAGTGGCCAAATGATGGCAGTGGCGGGTTCCTGCA 1432  
 |||||||  
 Db 840 ACGTGAAGCACCCTCCAAAGTGGCCAAATGATGGCAGTGGCGGGTTCCTGCA 899  
 |||||||  
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 |||||||  
 Db 900 GCCGTTCTGCGTGGGCTTCGCCGCTTCCTGCTTTTGTGCTTTATGCTATTTAC 959  
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 QY 1493 AACTAGTCTCTGCTGCGAG 1513  
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 Db 960 AACTAGTCTCTGCTGCGAG 980  
 |||||||  
 RESULT 14  
 AAT69188  
 ID AAT69188 standard; DNA: 4118 BP.  
 AC AAT69188;  
 XX  
 XX  
 DT 26-FEB-1998 (first entry)  
 DE Construct pGEM-htr containing RNA component of human telomerase.  
 XX  
 XX Human telomerase; quantification; tumour cell: pGEM-htr;  
 KM detection; micrometastasis; diagnosis; lymphoblastoma; leukaemia;  
 KM teratocarcinoma; melanoma; carcinoma; cancer; tumour; neuroblastoma;  
 KM rhabdomyosarcoma; leiomyosarcoma; lymphoma; RNA component; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH  
 XX  
 FT Key Location/Qualifiers  
 FT misc\_feature 12..975  
 /note="cDNA from RNA component of human telomerase"  
 FT  
 XX  
 PN MO9718322-A2.  
 XX  
 XX 22-MAY-1997.  
 PD  
 XX  
 PF 14-NOV-1996; 96WO-DE02183.  
 XX  
 PR 16-NOV-1995; 95DE-4042795.  
 XX  
 PA (DAHM/) DAHM M. W.  
 XX  
 PI Dahm MW;  
 XX  
 DR WPI: 1997-289298/26.  
 XX  
 PT Quantifying tumour cells in body fluid - by measuring RNA component  
 PT of telomerase after amplification, especially useful for early  
 PT diagnosis of metastasis  
 PT  
 PS Example 5; Fig 5; 46pp; German.  
 XX  
 CC The present sequence is the construct pGEM-htr, which comprises the  
 CC transcription vector pGEM-13zf(+) and the cDNA from the RNA  
 CC component of human telomerase. The construct was used in the  
 CC development of a novel method for quantifying tumour cells in a  
 CC body fluid. The method comprises specific amplification of the RNA  
 CC component of telomerase, and measuring the amount of amplified  
 CC nucleic acid. At least 1, preferably all 3 (AAT69173-75) standard  
 CC nucleic acids are present (at different concentrations) and are  
 CC co-amplified with telomerase DNA. The amplification products are  
 CC detected directly or via a label or by hybridisation with a  
 CC labelled oligonucleotide (AAT69184-87, 1 for each standard and 1 for  
 CC telomerase), and the amount of telomerase product compared with  
 CC that from the standards.  
 CC The method can be used to detect tumour cells, specifically  
 CC micrometastases, in a body fluid, particularly for the early  
 CC diagnosis of metastatic spread and for monitoring tumour therapy.  
 CC Typical tumour cells that can be quantified are micrometastases,

CC T cell lymphoblastoma or leukaemia (chronic myelogenous, and  
 CC chronic or acute lymphatic leukaemia), teratocarcinoma, melanoma,  
 CC carcinoma of lung, liver or prostate, cancer of colon or breast,  
 CC kidney, brain or adrenal tumours, neuroblastoma, rhabdomyosarcoma,  
 CC leiomyosarcoma and/or lymphoma.  
 CC  
 XX  
 SO Sequence 4118 BP; 991 A; 1032 C; 1094 G; 1001 T; 0 other;  
 Query Match 50.1%; Score 883.4; DB 18; Length 4118;  
 Best Local Similarity 97.6%; Pred. No. 1.2e-237;  
 Matches 950; Conservative 0; Mismatches 16; Indels 7; Gaps 5;  
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 |||||||  
 Db 14 GCCCGGGTTGCGAGGCTGGGCTGGAGGGGTGGGCTATTTTGTCTAACCTAA 73  
 |||||||  
 QY 854 CTGAGAGGCGCTAGAGCGCCGCTTTTGTCTCCCGCGCTTTTTCGCTGACTTT 913  
 |||||||  
 Db 74 CTGAGAGGCGCTAGAGCGCCGCTTTTGTCTCCCGCGCTTTTTCGCTGACTTT 133  
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 QY 914 CAGCGGGCGGAAAAAGCCTGCGCCTGCCGCTTCACCGCTTCATTTAGACAAACAAA 973  
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 Db 134 CAGCGGGCGGAAAAAGCCTGCGCCTGCCGCTTCACCGCTTCATTTAGACAAACAAA 193  
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 QY 974 ATGTGAGCTGCTGGCCGCTTCCCGGGGACCTGGCGGGGTCGCTGCCAGGC 1033  
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 Db 311 CCGCGAAGATTGGGCTCTGTCTACAGCCGCGGCTCTCGGGGCGAGGGCGAGTTGAGC 369  
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 QY 1153 CTTTCAAGGCGCGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212  
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 Db 370 GTTTCAGGCGCGAG 427  
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 Db 428 TGTGGAGCTGACACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487  
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 Db 488 GAAGCGGATCGTGCAGATCGTACACCGCTCGCGGAGTGGGGCTTGTGAACCCCAA 547  
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RESULT 15
AAT85371
ID AAT85371 standard; DNA; 962 BP.
XX
AC AAT85371;
XX
DT 15-APR-1998 (first entry)
XX
DE Human telomerase RNA component gene.
XX
KM Telomerase gene; transgenic organism; carcinogen; neoplastic growth;
XX cell growth; cell senescence; human; ss.
XX
OS Homo sapiens.
XX
PN M09735967-A2.
XX
PD 02-OCT-1997.
XX
PF 21-MAR-1997; 97MO-US05070.
XX
PR 28-MAR-1996; 96US-0623166.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
PI DePinho RA, Greider C, Lee H, Marhunda MB;
XX
XX WPI; 1997-489631/45.
XX
DR Non-human transgenic animal not expressing endogenous telomerase -
PT useful to test the carcinogenicity of a test compound, or to study
PT cell growth, division or senescence
XX
PS Disclosure: Fig 5: 58pp; English.
XX
XX
CC This sequence represents the human telomerase RNA component gene. This
CC sequence can be used in the transgenic organism of the invention. The
CC organism is a non-human transgenic organism in which at least one
CC endogenous telomerase gene encoding a telomerase component is altered and
CC telomerase activity is altered or is not expressed. The transgenic
CC organisms can be used as models to study telomerase activity. They can
CC also be used as a system to test compounds suspected of being
CC carcinogenic by exposing animals to the compound and determining
CC neoplastic growth as an indicator of carcinogenicity. The cells and
CC derived tissues are used to study cell growth and division and cell
CC senescence. The organisms are able to produce cells and tissues that, in
CC their wild type form, cannot be easily studied in vitro due to undergoing
CC small numbers of cell divisions.
XX
SQ Sequence 962 BP; 178 A; 257 C; 288 G; 239 T; 0 other;

Query Match 49.8%; Score 881.6; DB 18; Length 962;
Best local similarity 97.8%; Pred. No. 1.8e-2377;
Matches 947; Conservative 0; Mismatches 14; Indels 7; Gaps 5;
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Oy 1099 AAGAGTT--GGCTCTGTACAGCGCGGGGCTCTGCGGGGCGAGGCGAGTTCAAGGCTTTC 1157
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Oy 1158 AGCGCGGAGAGAGAGAGACGAGTCGAGTCCCGCGCGCGGCGGAGTTCCCTGAGCTGTCG 1217
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Oy 1218 GACGTGACCCAGGACTCGGCTCACACATGCAAGTTGCTTTCCTGTTGGTGGGGAGACG 1277
Db 415 GACGTGACCCAGGACTCGGCTCACACATGCAAGTTGCTTTCCTGTTGGTGGGGAGACG 474
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Db 475 CCGATGTCGCGCATCCGCTACACCCCTCGCGGAGTGGGGGCTTGTGACCCCAACCTG 534
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Db 955 ACAAGCTT 962
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Search completed: December 19, 2002, 14:53:39  
Job time : 312 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 : Search time 3240 Seconds  
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Title: US-09-601-267-1

Perfect score: 1765

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 1: gb\_da:\*
- 2: gb\_htg:\*
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- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
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- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
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- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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5	1719.6	97.4	2426	6	AR059196
6	1719.6	97.4	2426	6	AR075507
7	1719.6	97.4	2426	6	AR081664
8	1719.6	97.4	2426	6	AR161905
9	1661.2	94.1	2420	6	I31750
10	967.4	54.8	981	6	AR081665
11	966.4	54.8	981	6	AR028774
12	966.4	54.8	981	6	AR022166
13	965.8	54.7	981	6	AR4591
14	965.8	54.7	981	6	AR063825
15	965.8	54.7	981	6	AR079888
16	883.4	50.1	4118	6	A93963
17	881.6	49.9	962	6	A93962
18	867	49.1	867	6	AX019582
19	841.6	47.7	975	6	A93966
20	835.4	47.3	4118	6	A93964
21	835.2	47.3	975	6	A93967
22	830.4	47.0	975	6	A93965
23	582.8	33.0	598	6	HSU85256
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28	534.4	30.3	548	9	AF221907
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31	523.2	29.6	540	6	AR004985
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33	509.2	28.8	534	6	AR004987
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42	324.4	18.4	545	4	AF221906
43	317.6	18.0	547	4	AF221918
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# ALIGNMENTS

Result 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AX019547	AX019547	Sequence 1 from Patent WO9938964.	AX019547				human.			
1765 bp							Homo sapiens			
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
							Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
							1 (bases 1 to 1765)			
							Keith,W.N.			
							Promoter regions of the mouse and human telomerase rna component genes			

JOURNAL Patent: WO 9938964-A 1 05-AUG-1999:  
 KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)  
 FEATURES Location/Qualifiers  
 Source 1.1765  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 404 a 458 c 480 g 423 t  
 ORIGIN

Query Match 100.0%; Score 1765; DB 6; Length 1765;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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 ACCESSION AF047386  
 VERSION AF047386.1 GI:300555  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 1765)
AUTHORS Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
          Black,D.M. and Keith,W.N.
TITLE Cloning and characterization of human and mouse telomerase RNA gene
JOURNAL Promoter sequences
MEDLINE Oncogene 16 (10), 1345-1350 (1998)
PUBMED 9546436
REFERENCE 2 (bases 1 to 1765)
AUTHORS Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
          Black,D.M. and Keith,W.N.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
          Switchback Rd, Glasgow G61 1BD, UK
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BASE COUNT 404 a 458 c 480 g 423 t
ORIGIN
Query Match      100.0%; Score 1765; DB 9; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 661 ATGGAACCTTAAATTTCCCGTTCCCGCAACACAGACCGCGCGAGAGAGTCACTCAAGAG 720
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DB 1021 CGCCTGCCACGCCCCCGCAACCCCGCTGAGAGCGCGCGTGGGCGCGGCTTCTCCGAG 1080
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DB 1141 CGAGGTTCAAGGCTTTCAGGCGCGCAGGAAGAGGAAGGAGCGAGTCCCGCGCGGGCGC 1200
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LOCUS	ACOT8802/c	145829 bp	DNA
DEFINITION	Homo sapiens chromosome 3 clone R11-81656, WORKING DRAFT SEQUENCE.		
ACCESSION	ACOT8802		
VERSION	ACOT8802.11	GI:21397225	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T., Barberia,J., Benton,J., Blinagge,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,U., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P., Gabali,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Correll,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Llen,C., Liu,D., Liu,W., Loulsegod,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mahwinney,E., Mcleod,M.P., Meador,M., Mei,G., Metzker,M., Miler,G., Miler,Z., Mitchell,J., Mohabhat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,T., Mchabhat,K., Morgan,M., Morris,S., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okunoda,G., Oragunye,L., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Swatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalona,D., Vihson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.		
TITLE	Direct Submission		
JOURNAL	2 (bases 1 to 145829)		
REFERENCE	Unpublished		
AUTHORS	Worley,K.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
REFERENCE	3 (bases 1 to 145829)		
AUTHORS	Worley,K.C.		
TITLE	Direct Submission		

Oy	381	CCACGAGCCCAAGACAGATTTCTGCTAGACATGCTGCTGGAAATCAATTTTCACAA	420
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VERSION	AR016035.1	GI:3972312
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ORGANISM	Unknown.	
REFERENCE	Unclassified.	
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TITLE	Villegnon, B., Feng J., Funk W. and Andrews W.H.	
JOURNAL	Agents for the DNA-component of human telomerase	
FEATURES	Patent: US 5776679-A 3 07-JUL-1998;	
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ORIGIN		

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					Gaps
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Db 1141 AATCTCTCTGTGAATTCATTTTAAAGTAGTGAAGTGAACCGGCTGTGCTGCAGA 1200  
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OY 1620 AATATTAAATTAGAGATCTAAATGAACATTTGAAATTTGTTCTTTAATGATTCGG 1679  
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Db 2341 TTTATGCGAGGTTTGAAGTTCTTTTGAATAATTAAGTACCTTGGCATGACCTTGA 2400  
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ACCESSION AR075507  
VERSION AR075507.1 GI:10002257  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
Unclassified.  
1 (bases 1 to 2426)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5958680-A 4 28-SEP-1999;  
FEATURES  
source 1.2426  
BASE COUNT 620 a 575 c 650 g 581 t  
ORIGIN  
  
Query Match 97.4% Score 1719.6; DB 6; Length 2426;  
Best Local Similarity 99.1% Pred. No. 0;  
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 ACCESSION AR081664  
 VERSION AR081664.1 GI:10008390  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Unknown.  
 Unclassefied.  
 REFERENCE 1 (bases 1 to 2426)  
 AUTHORS Villepontoux,B. and Harley,C.  
 TITLE Assays for regulators of mammalian telomerase expression  
 JOURNAL Patent: US 5972605,A1 26-OCT-1999  
 FEATURES  
 source 1..2426  
 location/Qualifiers  
 BASE COUNT 620 a 575 c 650 g 581 t  
 ORIGIN

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;  
 Best Local Similarity 99.1%; Pred. No. 0; Mismatches 14; Indels 2; Gaps 2;  
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DEFINITION Sequence 3 from patent US 6258535.
ACCESSION AR161905
VERSION AR161905.1 GI:16228915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 3 10-JUL-2001;
FEATURES
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BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
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 VERSION I31750.1 GI:1822541  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2420)  
 AUTHORS Vilheponteau-Bry-Feng, J., Funk, W. and Andrews, W. H.  
 TITLE Mammalian telomerase  
 JOURNAL Patent: US 5583016-A 3 10-DEC-1996;  
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 BASE COUNT 620 a 572 c 647 g 581 t  
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D	1321	ATGGAATTTAATTTCCGCTTCCCGCAACGACCCCGCGAGAGTACTCTACGAG	1380
Q	721	ACCGCGAGATCAGCTTGCCCAATCCGTGCGGTGCGGCGCGCTCCCTTATACCGCA	780
D	1381	ACCGCGAGATCAGCTTGCCCAATCCGTGCGGTGCGGCGCGCTCCCTTATACCGCA	1440
Q	781	CTCGCCCGGACGACGACGCGGTTCGCGAGGTCGCGCTGGAGGGGTGGCCATTTT	840
D	1441	CTCGCCCGGACGACGCGGTTCGCGAGGTCGCGCTGGAGGGGTGGCCATTTT	1500
Q	841	TGTCTAACCTTAATCTAGAAAGGCGTAAAGCGCGCTTTTGTCTCCCGCGCGCTTTT	900
D	1501	TGTCTAACCTTAATCTAGAAAGGCGTAAAGCGCGCTTTTGTCTCCCGCGCGCTTTT	1560
Q	901	TCTCGCTGACTTTCAGCGGGCGGAAAAAGCTGCGGCTTCGCGCTTCACCGTTTCA	960
D	1561	TCTCGCTGACTTTCAGCGGGCGGAAAAAGCTGCGGCTTCGCGCTTCACCGTTTCA	1620
Q	961	GAGCAAAACAAAAATGTCACTGCTGCGCCCTTCGCGGAGACTGCGGCGGT	1020
D	1621	GAGCAAAACAAAAATGTCACTGCTGCGCCCTTCGCGGAGACTGCGGCGGT	1678
Q	1021	CGCTTCGCCAGCCCGGAAACCCCGCTGGAAGCGCGCGCTGCGCGCGCTTCGCGAG	1080
D	1679	CGCTTCGCCAGCCCGGAAACCCCGCTGGAAGCGCGCGCTGCGCGCGCTTCGCGAG	1737
Q	1081	GCACCTACTGCCACGCGGAAGAGTT-GGCTGTGTACGCGCGGCTCTCGGGGGGGAAG	1139
D	1738	GCACCTACTGCCACGCGGAAGAGTT-GGCTGTGTACGCGCGGCTCTCGGGGGGGAAG	1797
Q	1140	GCGAGGTTCAAGGCTTTCAGGCGCGAGAAAGAAAGAGAGGAGTCCCGCGCGCGG	1199
D	1798	GCGAGGTTCAAGGCTTTCAGGCGCGAGAAAGAAAGAGAGGAGTCCCGCGCGG	1854
Q	1200	CGATTCCTCGAGCTGTGGAGAGTGCACCAAGACTGGCTCACACATGCAATTTCCCTTC	1259
D	1855	CGATTCCTCGAGCTGTGGAGAGTGCACCAAGACTGGCTCACACATGCAATTTCCCTTC	1914
Q	1260	CTGTGTGTGGGGGGAAGCGCGATCGTCCGCTACCCCTCGCGGCGAGTGGGGGT	1319
D	1915	CTGTGTGTGGGGGGAAGCGCGATCGTCCGCTACCCCTCGCGGCGAGTGGGGGT	1974
Q	1320	TGTGAACCCCAAACTGACTGAGGCGCAAGTGTCTGCAAAATTTGGCAGGAGCTGAA	1379
D	1975	TGTGAACCCCAAACTGACTGAGGCGCAAGTGTCTGCAAAATTTGGCAGGAGCTGAA	2034
Q	1380	GCGACCTCCAAAGTGCGGCAAAATGAATGGCAGTACCGGGGTTCCTGAGCCGTTTC	1439
D	2035	GCGACCTCCAAAGTGCGGCAAAATGAATGGCAGTACCGGGGTTCCTGAGCCGTTTC	2094
Q	1440	CTGCGTGGGTTCTCCCGCTTTCGCGCTTTTGTGCTTATGTTGTATTAACATTTAG	1499
D	2095	CTGCGTGGGTTCTCCCGCTTTCGCGCTTTTGTGCTTATGTTGTATTAACATTTAG	2154
Q	1500	TTCTGCTCTGAGATTTTGTGAGGTTTTTGTCTCTCCAAAGTGAATCTGACCACTTC	1559

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D	2155	TTCTGCTCTGAGATTTTGTGAGGTTTTTGTCTCTCCAAAGTGAATCTGACCACTTC	2214
Q	1560	CCCTCAACGGGGTGTGGGAGAACAGTCATTTTGTGAGAGTCAATTTAACTTTAATG	1619
D	2215	CCCTCAACGGGGTGTGGGAGAACAGTCATTTTGTGAGAGTCAATTTAACTTTAATG	2274
Q	1620	AATTTTAAATTTGAATCATTAATGAACATTTGGAATTTGTCTTAAATGTCATCGG	1679
D	2275	AATTTTAAATTTGAATCATTAATGAACATTTGGAATTTGTCTTAAATGTCATCGG	2334
Q	1680	TTTATCCAGAGTTTGAAGTTTCTTTTGAATAAATTAAGACCTTGGCATGACTTGA	1739
D	2335	TTTATCCAGAGTTTGAAGTTTCTTTTGAATAAATTAAGACCTTGGCATGACTTGA	2394
Q	1740	CAGTAGATATAACCCGACACCTT 1765	
D	2395	CAGTAGATATAACCCGACACCTT 2420	
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DEFINITION	Sequence 2 from patent US 5972605.		
ACCESSION	AR081665		
VERSION	AR081665.1 GI:10008391		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 981)		
AUTHORS	Villeponteau B. and Harley C.		
TITLE	Assays for regulators of mammalian telomerase expression		
JOURNAL	Patent: US 5972605-A 2 26-OCT-1999;		
FEATURES	Location/Qualifiers		
source	1..981		
BASE COUNT	172 a 303 c 306 g 200 t		
ORIGIN			
Query Match 54.8%; Score 967.4; DB 6; Length 981;			
Best Local Similarity 99.8%; Pred. No. 4.7e-224;			
Matches 979; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
Q	534	CTGCACAGATGATAAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAG	593
D	1	CTGCACAGATGATAAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAG	60
Q	594	TGCGAAGTAAAGACGCAAGCCCTTCCGAGCTGCGGAAGGCAACGTCCTTCATG	653
D	61	TGCGAAGTAAAGACGCAAGCCCTTCCGAGCTGCGGAAGGCAACGTCCTTCATG	120
Q	654	GCGGGAATGAACCTTAAATTTCCCGTTCCCGCAACAGCCCGCGCGAGAGTACCTC	713
D	121	GCGGGAATGAACCTTAAATTTCCCGTTCCCGCAACAGCCCGCGCGAGAGTACCTC	180
Q	714	TCACGAGACCGCGAGAGTACCTTGGCCCAATTCGTGCGGTGCGGCGCGCTCCCTTAT	773
D	181	TCACGAGACCGCGAGAGTACCTTGGCCCAATTCGTGCGGTGCGGCGCGCTCCCTTAT	240
Q	774	AAGCCACTGCGCGCGACGCAACCGGTTGCGAGAGTGGGCTGGAGAGGTTGTGAC	833
D	241	AAGCCACTGCGCGCGACGCAACCGGTTGCGAGAGTGGGCTGGAGAGGTTGTGAC	300
Q	834	CATTTTGTCTAACCCTTAAGAGGCGTAAAGGCGCTGCTTTCCTCCCGCGG	893
D	301	CATTTTGTCTAACCCTTAAGAGGCGTAAAGGCGCTGCTTTCCTCCCGCGG	360
Q	894	CTGTTTCTCCGCTGACTTTCAGCGGGCGGAAAGCTGCGGCTGCGGCTTCACACCTT	953
D	361	CTGTTTCTCCGCTGACTTTCAGCGGGCGGAAAGCTGCGGCTGCGGCTTCACACCTT	420
Q	954	CATTCTAGAGCAAAACAAAAATGTCACTGCTGCGCCGCTTCGCCGCGGAGACTGC	1013

Query March	54.88;	Score 966.4;	DB 6;	Length 981;
Best Local Similarity	99.7%;	Pred. No. 8,2e-224;		
Matches 978;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1
QY 534	CTGCAGAGATAGCAAAAAAGGCCCTGTATACCTCAATTAGTTTACACCTTTAAAGAGG	593		
Db 1	CTGCAGAGATAGCAAAAAAGGCCCTGTATACCTCAATTAGTTTAAAGAGG	60		
QY 594	TGCGAATTAAGACGCAAAAGCCTTTCCGCGAGCTCGGAAGGGCAAGCTCTTCTCATG	653		
Db 61	TGCGAATTAAGACGCAAAAGCCTTTCCGCGAGCTCGGAAGGGCAAGCTCTTCTCATG	120		
QY 654	GCCGGAAATGGAACCTTTAAATTCCCGTTCCCGCCCAACCAAGCCGCCCGAGAGAGTGATC	713		

RESULT 12					
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LOCUS	AX022166	981 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 5 from Patent EP0953042.				
ACCESSION	AX022166				
VERSION	AX022166.1	GI:10045843			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unidentified.				
REFERENCE	1 (bases 1 to 981)				
AUTHORS	Andrews, W. H., Villeponteau, B., Adams, R. R. and Feng, J.				
TITLE	Methods and reagents for regulating telomere length and telomerase				

activity  
 Patent: EP 0953042-A 5 03-NOV-1999;  
 GERON CORP (US)  
 Location/Qualifiers  
 FEATURES  
 source  
 1. .981  
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 /db\_xref="taxon:32644"  
 267. .715  
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 RIBONUCLEOPROTEIN"  
 BASE COUNT 172 a 303 c 305 g 200 t 1 others  
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Query Match 54.8%; Score 966.4; DB 6; Length 981;  
 Best Local Similarity 99.7%; Pred. No. 8.2e-224;  
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 534 CTCGACAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAG 593  
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OY 594 TCGGAAGTAAGACGCAAAACCTTTCCCGAGCTGGCGAAGGGCAACGTTCTTCATG 653  
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 DB 61 TCGGAAGTAAGACGCAAAACCTTTCCCGAGCTGGCGAAGGGCAACGTTCTTCATG 120  
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OY 654 GCGGAAATGGAAGTTAATTTCCCGTCCCGCAACGACCCCGCGAGAGAGTCACTC 713  
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 DB 121 GCGGAAATGGAAGTTAATTTCCCGTCCCGCAACGACCCCGCGAGAGAGTCACTC 180  
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OY 714 TCACGAGAGCCGAGAGTACGCTTGCCCAATCGTGCGGTGGCGCCCTCCCTTTAT 773  
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 DB 181 TCACGAGAGCCGAGAGTACGCTTGCCCAATCGTGCGGTGGCGCCCTCCCTTTAT 240  
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OY 774 AACCGACTGCCCGGACGCAACCGGGTTGCGAAGGGTGGCTGGAGGGGTGTGGC 833  
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 DB 241 AACCGACTGCCCGGACGCAACCGGGTTGCGAAGGGTGGCTGGAGGGGTGTGGC 300  
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OY 834 CATTTTGTCTAACCTTAAGAAAGGCGTGGCGGCTTTTGTCTCCCGCGCG 893  
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 DB 301 CATTTTGTCTAACCTTAAGAAAGGCGTGGCGGCTTTTGTCTCCCGCGCG 360  
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OY 894 CTGTTTTTCTCGTGAATTCACGCGGCGGAAAGCTTCGCGCTTCACCGTT 953  
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 DB 361 CTGTTTTTCTCGTGAATTCACGCGGCGGAAAGCTTCGCGCTTCACCGTT 420  
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OY 954 CATTTAGAGCAAAATAATGTCAAGTGTGCGCCGTTCCCGGAGACTGC 1013  
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 DB 421 CATTTAGAGCAAAATAATGTCAAGTGTGCGCCGTTCCCGGAGACTGC 480  
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OY 1014 GCGGGGTGCGCTGCCAGCCCGCAACCCGCGTGGAGGCGGCGGTGCGCGGGGCTTC 1073  
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 DB 481 GCGGGGTGCGCTGCCAGCCCGCAACCCGCGTGGAGGCGGCGGTGCGCGGGGCTTC 540  
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OY 1074 TCCGAGAGCACTACTTCCACCGCGAAGATT-GGCTGTGTACAGCGCGGGTCTTCGCG 1132  
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 DB 541 TCCGAGAGCACTACTTCCACCGCGAAGATTGGCTGTGTACAGCGCGGGTCTTCGCG 600  
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OY 1133 GCGGAGGCGAGGTTACAGGCTTTACAGCGCGCAAGAAAGAAAGAGAGAGTCCCGCG 1192  
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 DB 601 GCGGAGGCGAGGTTACAGGCTTTACAGCGCGCAAGAAAGAGAGAGTCCCGCG 660  
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OY 1193 GCGGGGCGGATTCCTGAGCTGTGGAGCGTGCACCAAGATCGGGTCAACATTCAGATT 1252  
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 DB 661 GCGGGGCGGATTCCTGAGCTGTGGAGCGTGCACCAAGATCGGGTCAACATTCAGATT 780  
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OY 1253 CCGTTTCCTGTTGGTGGGGAAGCGCGATCGTGCGATCCGTACACCCCTCGCGGCGAGT 1312  
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 DB 721 CCGTTTCCTGTTGGTGGGGAAGCGCGATCGTGCGATCCGTACACCCCTCGCGGCGAGT 780  
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RESULT 13  
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 DEFINITION Sequence 1 from Patent WO9845450.  
 ACCESSION A84591  
 VERSION A84591.1 GI:6733507  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 981)  
 AUTHORS Atkinson,E.M. and Kealey,J.T.  
 TITLE PURIFIED TELOMERASE  
 JOURNAL Patent: WO 9845450-A 1 15-OCT-1998;  
 GERON CORP (US)  
 FEATURES  
 source  
 1. .981  
 Location/Qualifiers  
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 /db\_xref="taxon:32644"  
 266. .716  
 /product="HTR"  
 /note="RNA COMPONENT OF HUMAN TELOMERASE (HTR)"  
 BASE COUNT 172 a 303 c 305 g 200 t 1 others  
 ORIGIN

Query Match 54.7%; Score 965.8; DB 6; Length 981;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-223;  
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 534 CTCGACAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAG 593  
 |||||||  
 DB 1 CTCGACAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAG 60  
 |||||||

OY 594 TCGGAAGTAAGACGCAAAACCTTTCCCGAGCTGGCGAAGGGCAACGTTCTTCATG 653  
 |||||||  
 DB 61 TCGGAAGTAAGACGCAAAACCTTTCCCGAGCTGGCGAAGGGCAACGTTCTTCATG 120  
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OY 654 GCGGAAATGGAAGTTAATTTCCCGTCCCGCAACGACCCCGCGAGAGAGTCACTC 713  
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 DB 121 GCGGAAATGGAAGTTAATTTCCCGTCCCGCAACGACCCCGCGAGAGAGTCACTC 180  
 |||||||

OY 714 TCACGAGAGCCGAGAGTACGCTTGCCCAATCGTGCGGTGGCGCCCTCCCTTTAT 773  
 |||||||  
 DB 181 TCACGAGAGCCGAGAGTACGCTTGCCCAATCGTGCGGTGGCGCCCTCCCTTTAT 240  
 |||||||

OY 774 AACCGACTGCCCGGACGCAACCGGGTTGCGAAGGGTGGCTGGAGGGGTGTGGC 833  
 |||||||  
 DB 241 AACCGACTGCCCGGACGCAACCGGGTTGCGAAGGGTGGCTGGAGGGGTGTGGC 300  
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OY 834 CATTTTGTCTAACCTTAAGAAAGGCGTGGCGGCTTTTGTCTCCCGCGCG 893  
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 DB 301 CATTTTGTCTAACCTTAAGAAAGGCGTGGCGGCTTTTGTCTCCCGCGCG 360  
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OY 894 CTGTTTTTCTCGTGAATTCACGCGGCGGAAAGCTTCGCGCTTCACCGTT 953  
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 DB 361 CTGTTTTTCTCGTGAATTCACGCGGCGGAAAGCTTCGCGCTTCACCGTT 420  
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OY 954 CATTTAGAGCAAAATAATGTCAAGTGTGCGCCGTTCCCGGAGACTGC 1013  
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Db 421 CATTTAGAGCAAAATAATGTCAGCTGCTGGCCCTTGCCTCCGCGGAGACCTGC 480
Oy 1014 GCGGGGTGCTGGCCAGCCCGGACCCCGCTGTGAGGCGCGGTGGCCCGGGCTTC 1073
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Db 781 GGGGGCTTGTGAACCCCGCAAACTGACTGACTGGGCACTGTGTGCAAAATTGGCAGAG 840
Oy 1373 ACGTGAAGGACCTCCAAAGTGCGCCAAATGAATGGGAGTGAAGCGGGGTGCTGGA 1432
Db 841 ACGTGAAGGACCTCCAAAGTGCGCCAAATGAATGGGAGTGAAGCGGGGTGCTGGA 900
Oy 1433 GCGGTTCTGTGCGTGGTTCCTCCGTTTCCGTTTGTGTGCTTTTATGTTGATTATAC 1492
Db 901 GCGGTTCTGTGCGTGGTTCCTCCGTTTCCGTTTGTGTGCTTTTATGTTGATTATAC 960
Oy 1493 AACTTAGTTCCTGCTCTGAG 1513
Db 961 AACTTAGTTCCTGCTCTGAG 981

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RESULT 14
LOCUS AR063825 981 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5846723.
ACCESSION AR063825
VERSION AR063825.1 GI:5993133
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Kim, N.Moo., Wu, F., Kealey, J.T., Pruzan, R., and Weinrich, S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 1 08-DEC-1998;
FEATURES
Location/Qualifiers
1..981
BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

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Query Match 54.7% Score 965.8; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 1,1e-223;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Oy 534 CTCGACAGATGAAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAG 593
Db 1 CTCGACAGATGAAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAG 60
Oy 594 TCGGAAGTAAAGACGCTTTCCTCGAGAGTGGGAGGGAAGCTCTTCTCATG 653
Db 61 TCGGAAGTAAAGACGCTTTCCTCGAGAGTGGGAGGGAAGCTCTTCTCATG 120
Oy 654 GCGGAATGGAACCTTATTTCCGTTCCCGCAACAGCCCGCGAGAGATGACTC 713

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Db 181 TCACGAGACCGCGAGATGCTTGGCCAAATCCGTGCGTGGCGCGCTTCTTAT 240
Oy 774 AAGCGACTGCGCCCGGACGCGACCGGGTTGCGAGAGGTGGGTGGGTGGTGGC 833
Db 241 AAGCGACTGCGCCCGGACGCGACCGGGTTGCGAGAGGTGGGTGGGTGGTGGC 300
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Oy 894 CTGTTTCTGCTGACTTTCAGCGGGCGGAAAGCGCTGGGCTGCGGCTTCCACGTT 953
Db 361 CTGTTTCTGCTGACTTTCAGCGGGCGGAAAGCGCTGGGCTGCGGCTTCCACGTT 420
Oy 954 CATTTAGAGCAAAATAATGTCAGCTGTGCGCCCTTCCCGCTCCGAGACCTGC 1013
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Oy 1014 GCGGGCTGCTGCGCCAGCGCCCGAAACCGCGCTGAGGCGCGGTGGCGCGGCTTC 1073
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Db 841 ACGTGAAGGACCTCCAAAGTGCGCCAAATGAATGGGAGTGAAGCGGGGTGCTGGA 900
Oy 1433 GCGGTTCTGTGCGTGGTTCCTCCGTTTCCGTTTGTGTGCTTTTATGTTGATTATAC 1492
Db 901 GCGGTTCTGTGCGTGGTTCCTCCGTTTCCGTTTGTGTGCTTTTATGTTGATTATAC 960
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Db 961 AACTTAGTTCCTGCTCTGAG 981

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RESULT 15
LOCUS AR079888 981 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5968506.
ACCESSION AR079888
VERSION AR079888.1 GI:1006641
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Weinrich, S.L., Atkinson, E.M. III, Lichtsteiner, S.P., Vassero, A.P.,
TITLE Purified telomerase

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JOURNAL Patent: US 5968506-A 1 19-OCT-1999;  
 FEATURES Location/Qualifiers  
 source 1. 981  
 BASE COUNT 172 a 303 c 305 g 200 t 1 others  
 ORIGIN

Query Match 54.7%; Score 965.8; DB 6; Length 981;  
 Best local similarity 99.7%; Pred. No. 1.1e-223;  
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 534 CTCGAGAGATAGAAAAAAGGCCCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593  
 Db 1 CTCGAGAGATAGAAAAAAGGCCCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60  
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 QY 654 GCCGAAATGGAATTAATTTCCCGTCCCGCAACAGCCGCGGAGAGAGTACTC 713  
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 Db 301 CATTTTGTCTAACCTTAAGGAGGCGTAAAGGCGCGCTTGTGCTCCCGGCGG 360  
 QY 894 CTGTTTTCTCGCTGACTTTACGCGGGGCAAAAGCCTCGCCCTGCACCGTT 953  
 Db 361 CTGTTTTCTCGCTGACTTTACGCGGGGCAAAAGCCTCGCCCTGCACCGTT 420  
 QY 954 CATTCTAGACAAACAAAATGTCACTGCTGGCCGTTCCCGGAGCCTGC 1013  
 Db 421 CATTCTAGACAAACAAAATGTCACTGCTGGCCGTTCCCGGAGCCTGC 480  
 QY 1014 GCGGGGTGCGCTGCGCCGACCCGCAACCCGCGTGGAGGCGGCGGCGGCTTC 1073  
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 Db 841 ACGTGAAGGACCTCCAAAGTGGCCAAATGATGGCAGTGAGCCGGGGTGGCTGGA 900  
 QY 1433 GCGTTTCTTGTGGTGGGTTCTCCGCTTTGTTGCTTTATGTTGTATTAC 1492  
 Db 901 GCGTTTCTTGTGGTGGGTTCTCCGCTTTTGTGCTTTATGTTGTATTAC 960  
 QY 1493 AACTTACTTCTGCTGTCAG 1513  
 Db 961 AACTTACTTCTGCTGTCAG 981

Search completed: December 19, 2002, 14:12:02  
 Job time : 3320 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 63 Seconds  
(without alignments)  
8591.817 Million cell updates/sec

Title: US-09-601-267-1

Perfect score: 1765

Sequence: 1 agctactcaggagcgtcaga.....gatatacccccacaaagctt 1765

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 443362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/pdata/1/1na/5B.COMB.seq:\*  
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6: /cgn2\_6/pdata/1/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1719.6	97.4	2426	1 US-08-482-115B-3	Sequence 3, Appl1
2	1719.6	97.4	2426	2 US-08-660-678A-3	Sequence 3, Appl1
3	1719.6	97.4	2426	2 US-08-472-802C-4	Sequence 4, Appl1
4	1719.6	97.4	2426	2 US-08-714-482-1	Sequence 1, Appl1
5	1719.6	97.4	2426	3 US-08-998-443-3	Sequence 3, Appl1
6	1719.6	97.4	2426	4 US-09-060-523-3	Sequence 3, Appl1
7	1661.2	94.1	2420	1 US-08-330-123A-3	Sequence 3, Appl1
8	1661.2	94.1	2420	4 US-09-580-517-3	Sequence 3, Appl1
9	1640.8	93.0	2425	2 US-08-485-778-1	Sequence 3, Appl1
10	1640.8	93.0	2425	3 US-08-520-550A-1	Sequence 1, Appl1
11	967.4	54.8	981	2 US-08-714-482-2	Sequence 2, Appl1
12	966.4	54.8	981	2 US-08-710-249-5	Sequence 5, Appl1
13	966.4	54.8	981	4 US-09-220-157A-5	Sequence 5, Appl1
14	965.8	54.7	981	2 US-08-770-565-1	Sequence 1, Appl1
15	965.8	54.7	981	2 US-08-833-377-1	Sequence 1, Appl1
16	965.8	54.7	981	3 US-08-838-545-22	Sequence 22, Appl1
17	965.8	54.7	981	4 US-09-349-513-22	Sequence 22, Appl1
18	910.8	51.6	965	3 US-08-520-550A-44	Sequence 44, Appl1
19	881.6	49.9	962	4 US-09-018-125-1	Sequence 1, Appl1
20	546.4	31.0	560	1 US-08-482-115B-1	Sequence 1, Appl1
21	546.4	31.0	560	2 US-08-660-678A-1	Sequence 1, Appl1
22	546.4	31.0	560	2 US-08-472-802C-2	Sequence 2, Appl1
23	546.4	31.0	560	3 US-08-998-443-1	Sequence 1, Appl1
24	546.4	31.0	560	4 US-09-060-523-1	Sequence 1, Appl1
25	526.4	29.8	540	1 US-08-676-967-6	Sequence 6, Appl1
26	526.4	29.8	540	1 US-08-676-974-6	Sequence 6, Appl1
27	526.4	29.8	540	2 US-09-098-487-6	Sequence 6, Appl1

28	523.2	29.6	540	1 US-08-676-967-7	Sequence 7, Appl1
29	523.2	29.6	540	1 US-08-676-967-8	Sequence 8, Appl1
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31	523.2	29.6	540	1 US-08-676-974-8	Sequence 8, Appl1
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35	509.2	28.8	538	1 US-08-676-974-9	Sequence 9, Appl1
36	509.2	28.8	538	2 US-09-098-487-9	Sequence 9, Appl1
37	488	27.6	554	1 US-08-330-123A-1	Sequence 1, Appl1
38	488	27.6	554	4 US-09-580-517-1	Sequence 1, Appl1
39	474.6	26.9	559	2 US-08-485-778-2	Sequence 2, Appl1
40	474.6	26.9	559	3 US-08-520-550A-2	Sequence 2, Appl1
41	472.4	26.8	486	3 US-08-630-019A-31	Sequence 31, Appl1
42	468	26.5	534	2 US-09-098-487-11	Sequence 11, Appl1
43	437.4	24.8	451	4 US-09-645-713-1	Sequence 1, Appl1
44	408.2	23.1	448	3 US-08-520-550A-45	Sequence 45, Appl1
45	367	20.8	444	3 US-08-873-709-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-482-115B-3  
; Sequence 3, Application US/08482115B  
; Patent No. 5776679  
; GENERAL INFORMATION:  
; APPLICANT: Villaponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Assays for the RNA Component of Human  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,115B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000830US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2426 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: Single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-482-115B-3

Query Match 97.4%; Score 1719.6; DB 1; Length 2426;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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 DB 662 AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCCGGAGGACAGAGTTGACAGT 720  
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QY 61 AGCGGAGTACGCGGCTGAGACAGAGAAATCGCTTGAACCCCGGAGGACAGAGTTGACAGT 120  
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QY 181 CAGACACTTTTAAAGCAAGTCAATATTTGAACGCTTTCTTTCTTAATTAAGGAG 240  
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 DB 841 CAGACACTTTTAAAGCAAGTCAATATTTGAACGCTTTCTTTCTTAATTAAGGAG 900  
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QY 241 ATTTCAGTCTTAAGATTATATGATAGTTACCTTGAATTAAGGACATCGCTCTCA 300  
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DB 1861 CGATTCCTGAGCTGTGGGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
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QY 1440 CTGCTGGTGTCTCCGCTCTCCGCTTTTGTGCTTTATGTTGTTATTCACATTAG 1499  
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DB 2101 CTGCTGGTGTCTCCGCTCTCCGCTTTTGTGCTTTATGTTGTTATTCACATTAG 2160  
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QY 1500 TTCTGCTCTGCAAGATTGTTGAGGTTTCTCTTCCCAAGGAGAGATCTGACAGTC 1559  
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DB 2161 TTCTGCTCTGCAAGATTGTTGAGGTTTCTCTTCCCAAGGAGAGATCTGACAGTC 2220  
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DB 2281 AATATTTATTTAGAGATCTTAAATGAACATTTGGAATTTGCTCTTAAATGTCATCG 2340  
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RESULT 2  
 US-08-660-678A-3  
 ; Sequence 3, Application US/08660678A  
 ; Patent No. 5837857  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Villefontaine, Bryant  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Funk, Walter  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Mammalian Telomerase  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678A  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2426 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-660-678A-3

Query Match 97.4%; Score 1719.6; DB 2; Length 2426;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Db 662 AGCTACTCAGAGAGGCTGAGACAGAGATCGCTGAACCGGGGAGAGGTTGAGTG 720  
61 AGCGGATCAGCGCCACTAGATCCATCCAGCGCTGGCGAAGAGAGAGACTCCGTCTCA 120  
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Db 901 ATTCACTCTTAAGATTAAATAGTAGTACACTGATTAAAGCCATCCCTGCTCA 960  
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Db 961 AGGAGAAGCTGGGAAGGCAATCTTAAGAAAAAGGGGCAAGGTTGCACTCGAGCCATC 1020  
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Db 1021 CCACTAGCGGAGACAAGATTCGCTGATGACAGTCTGCTGGGAATCATTTTACAA 1080  
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Db 1081 AGTTCTCAAAAAATGTGATGATCAAACTAGGAATTAGTGTCTGTCTTAAGGCCCTA 1140  
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601 TAAAGACGCAAGCCCTTCCCGGACGTGGGGAAGGCAAGCTCCCTTCCTATGCGCGAA 660

1261 TAAAGACGCAAGCCCTTCCCGGACGTGGGGAAGGCAAGCTCCCTTCCTATGCGCGAA 1320  
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Db 1321 ATGGAACTTAATTTCCGCTTCCCGCAACAGACCCCGCGAGAGTACTCTACGAG 1380  
721 AGCGGAGAGTCAAGCTTGGCCCAATCGTGGGTGGGGCGGCTCCCTTTAAGCCGA 780  
Db 1381 AGCGGAGAGTCAAGCTTGGCCCAATCGTGGGTGGGGCGGCTCCCTTTAAGCCGA 1440  
781 CTCGCCGCGAGCGCACCGGCTTGGCGAGGTTGGGCTGGAGGGGTGGTGCATTTT 840  
Db 1441 CTCGCCGCGAGCGCACCGGCTTGGCGAGGTTGGGCTGGAGGGGTGGTGCATTTT 1500  
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901 TCTCGCTGACTTTCAGCGGGCGGAAAGCGCTGGCGCTTCACCGTTCAATTTA 960  
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Db 1681 CGCTGCGCCAGCCCGCGAAGCCCGCTGGAAGCGCGGCTCGCGGGCTTCTCCGAG 1740  
1081 GCACCTACTGCAACGCGGAAAGT--GGCTGTGTCAGCGCGGGGTCTCGGGGGGAG 1139  
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1140 GCGAGGTTCAAGGCTTTCAGCGCGCGAGAAAGAAAGAGAGAGTCCCGCGCGCGG 1199  
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1200 CGATTCTCGAGCTGTGGAGCTGACCCAGAGACTGGCTCACATATGCAATTCGCTTTC 1259  
Db 1861 CGATTCTCGAGCTGTGGAGCTGACCCAGAGACTGGCTCACATATGCAATTCGCTTTC 1920  
1260 CTGTGTGGGGGGAAGCGCGAATCGTGGCATCCGTCACCCCGCGCGAGGGGGCT 1319  
Db 1921 CTGTGTGGGGGGAAGCGCGAATCGTGGCATCCGTCACCCCGCGCGAGGGGGCT 1980  
1320 TGTGAACCCCAAACTGACTGAGTGGCCAGTGTGCTCAAAATTTGGCAGAGACTGAA 1379  
Db 1981 TGTGAACCCCAAACTGACTGAGTGGCCAGTGTGCTCAAAATTTGGCAGAGACTGAA 2040  
1380 GGCACCTCCAAAGTCGGCCAAATGAAATGAGGCAAGTGGCGGGGTGCTGGAGCCGTTTC 1439  
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RESULT 3  
US-08-472-802C-4  
; Sequence 4, Application US/08472802C  
; Patent No. 5958680  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,802C  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15389-000820  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ. ID NO. 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2426 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-472-802C-4

Query Match 97.4%; Score 1719.6; DB 2; Length 2426;  
Best local Similarity 99.1%; Pred. No. 0;  
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Qy 1 AGCTACTGAGGGCTGACACAGAGATCGCTTGACCCGGGAGGAGAGTTGCAGTG 60  
Db 662 ACCTACTGAGGGCTGACACAGAGATCGCTTGACCCGGGAGGAGAGTTGCAGTG 720  
Qy 61 ACCGAGATCAGCCACTAGACTCATCCAGCTGGGGGAAAGACAGACTCCGCTCA 120  
Db 721 ACCGAGATCAGCCACTAGACTCATCCAGCTGGGGGAAAGACAGACTCCGCTCA 780  
Qy 121 AAAAAAATGTTACATTTATGGTGATTAATCTCCCTCTTTTACCTCAAGACA 180  
Db 781 AAAAAAATGTTACATTTATGGTGATTAATCTCCCTCTTTTACCTCAAGACA 840  
Qy 181 CAGCACTACTTAAGCAAGTCATGATGAACGCCCTTCTTCCATTAAGAGGAG 240  
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Db 841 CAGCACTACTTAAGCAAGTCATGATGAACGCCCTTCTTCCATTAAGAGGAG 900  
Qy 241 ATTGAGTCTTAAAGATTAATTAATGATAGTACTTACACTTGATTAAGCCATCTGTCTCA 300  
Db 901 ATTGAGTCTTAAAGATTAATTAATGATAGTACTTACACTTGATTAAGCCATCTGTCTCA 960  
Qy 301 AGGAGAGCTGAGAGAGGCAATTTAGGSAAGAGGGGAGGGTGGAACTCGAGCATC 360  
Db 961 AGGAGAGCTGAGAGAGGCAATTTAGGSAAGAGGGGAGGGTGGAACTCGAGCATC 1020  
Qy 361 CCACTAGCCGAGACAAGATTCGTGTAGTACAGTGCCTCGTGGAAATCTATTTCACAA 420  
Db 1021 CCACTAGCCGAGACAAGATTCGTGTAGTACAGTGCCTCGTGGAAATCTATTTCACAA 1080  
Qy 421 AGTTCTCCAAAAATGATGATCAAACTAGCAATTAATGTTCTGTGTCTTAAAGCCCTA 480  
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Db 1141 AATCTCTCTGTAATTCATTTTAAAGTATGAGTACGAGTGAACCGCTGTGTGACGA 1200  
Qy 541 GGAATAGAAAAAGGCCCTGTGATACCTCAAGTTACCTTTAAAGAGTCGAGAG 600  
Db 1201 GGAATAGAAAAAGGCCCTGTGATACCTCAAGTTACCTTTAAAGAGTCGAGAG 1260  
Qy 601 TAAAGACGCAAGCCCTTCCGAGAGTGGGAGGAGGCAAGCTCTCTCTATGCGCGGA 660  
Db 1261 TAAAGACGCAAGCCCTTCCGAGAGTGGGAGGAGGCAAGCTCTCTCTATGCGCGGA 1320  
Qy 661 ATGGAACCTTAATTTCCGCTTCCCGCAACAGCCCGCCGAGAGTGAATCTCACAG 720  
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Qy 721 AGCCGAGAGTCAAGCTTGGCCAAATCCGTGGTGGGCGGCGCTTCTTATTAAGCCGA 780  
Db 1381 AGCCGAGAGTCAAGCTTGGCCAAATCCGTGGTGGGCGGCGCTTCTTATTAAGCCGA 1440  
Qy 781 CTGCGCCGCGAGCGCAGCGGCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
Db 1441 CTGCGCCGCGAGCGCAGCGGCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Qy 841 TGCTAAACCTTAAGTGAAGAGGGGTAGGGCGCTGTGCTTGTCTCCCGCGCGCTGTTT 900  
Db 1501 TGCTAAACCTTAAGTGAAGAGGGGTAGGGCGCTGTGCTTGTCTCCCGCGCGCTGTTT 960  
Qy 901 TCTGCTGACTTAAAGCGGGGAGAAAGCCTCGGCTCGGCGCTTCCACCGCTTCAATTTCTA 960  
Db 1561 TCTGCTGACTTAAAGCGGGGAGAAAGCCTCGGCTCGGCGCTTCCACCGCTTCAATTTCTA 1620  
Qy 961 GAGCAACAAAAAATGTCACAGCTGTGCGCCGCTTCCGCGGAGCTCGGCGGAGT 1020  
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Qy 1021 CGCCTGCCAGCCCGGAAACCGCGCTGAGAGGCGGCGCTCGGCGGAGTCTTCCGGAG 1080  
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Qy 1081 GCACCTACCTGCGACCGGAGAAATTTTGGCTGTGTCAGCCGCGGCTTCTCGGGGCGAGG 1139  
Db 1741 GCACCTACCTGCGACCGGAGAAATTTTGGCTGTGTCAGCCGCGGCTTCTCGGGGCGAGG 1800  
Qy 1140 GCGAGGTTGAGGCTTTCAGAGCGCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1199  
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Db 1861 CGATTCCTGAGCTGTGAGAGTGAACCCAGAGACTCGGCTCAACATGACAGTTCGCTTTC 1920  
Qy 1260 CTGTTGTTGGGGGAAAGCGGATCGTGGGCAATCCGCTGACACCTCGCGCGGAGTGGGCT 1319  
Db 1921 CTGTTGTTGGGGGAAAGCGGATCGTGGGCAATCCGCTGACACCTCGCGCGGAGTGGGCT 1980



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Qy 901 TGTCTAACCTTAAGTGAAGAGGAGTTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 960
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Qy 1140 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 1199
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Db 1801 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 1860
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Qy 1200 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 1259
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Db 1861 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 1920
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Qy 1260 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 1319
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Qy 1320 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 1379
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Qy 1740 GAGCAACAAATATGTCAGCTTGGCCATCCGTGCGTGGCGGCGCTCCCTTTATAGCCGA 2400
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Db 2401 CAGTGAATATTAACCCCGCAGAGCTT 2426

RESULT 5
US-08-998-443-3
; Sequence 3, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-998-443-3

Query Match 97.4%; Score 1719.6; DB 3; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Qy 1 AGTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCGGAGGAGCAGAGTTGCAGTG 60
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Db 662 AGTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCGGAGGAGCAGAGTTGCAGTG 720
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Qy 61 AGCGAGATCAGCGCATAGCTCCATCCAGCTGGGCGGAAGAGCAGAGTCCGTCTCA 120
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Db 721 AGCGAGATCAGCGCATAGCTCCATCCAGCTGGGCGGAAGAGCAGAGTCCGTCTCA 780
|||
Qy 121 AAAAAAAAAAATCGTCAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 180
|||
Db 781 AAAAAAAAAAATCGTCAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 840
|||
Qy 181 CAGCAGTCTTTAAGCAAGTCAATGATTGAAGAGCCTTTCTTCTTAATAAAGGAG 240
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Db 841 CAGCAGTCTTTAAGCAAGTCAATGATTGAAGAGCCTTTCTTCTTAATAAAGGAG 900
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DB 901 ATTCACTCTTAAGATTAAATAGTAGTACACTTGATTAAACCATCTCTGCTCA 960
OY 301 AGAGAAAGCTGGAGAAGCACTTCTAAGGAAAAAGGGGCTGGAACTCGAGCCATC 360
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DB 1021 CCAGTAGCCGAGACAAAGATTCTGATAGTGTGCTGCGGGAATCTATTTTCACA 1080
OY 421 AGTTCTCAAAAAATGTGATGATCAAAACTAGGAATTAAGTTCTGTCTTAAGCCCTA 480
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DB 1081 AGTTCTCAAAAAATGTGATGATCAAAACTAGGAATTAAGTTCTGTCTTAAGCCCTA 1140
OY 481 AATCTCTCTGTGAATTCATTTTAAAGTATGCGAGGTGAACCCGCTGTGCTGACA 540
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DB 1141 AATCTCTCTGTGAATTCATTTTAAAGTATGCGAGGTGAACCCGCTGTGCTGACA 1200
OY 541 GGATGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGTGGAG 600
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DB 1201 GGATGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTAAAGAGTGGAG 1260
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OY 781 CTCGCCCGGACAGCGACCGGCTTGGCGAGGCTGGAGGGGTGGTGGCCATTTT 840
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DB 1441 CTCGCCCGGACAGCGACCGGCTTGGCGAGGCTGGAGGGGTGGTGGCCATTTT 1500
OY 841 TGTCTAACCCTTAAGTGAAGAGCGCTAGGCGCCGCTTTCTCTCCCGCGCTGTTT 900
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DB 1741 GCACCTACGCGACCGCGGAAGACTTGTGTCTGCGCGGCTTCTCGGCGGAGAG 1800
OY 1140 GCGAGGTTGAGGCTTTTCAAGCGCGAGAAAGAAAGAGAGAGTCCCGCGCGGCGG 1199
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DB 1801 GCGAGGTTGAGGCTTTTCAAGCGCGAGAAAGAAAGAGAGTCCCGCGCGGCGG 1860
OY 1200 CGATTCTCTGAGCTGTGAGACGTGCACCCAGAGACTGTGGCTCAACATGAGATTGCTTTC 1259
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DB 1861 CGATTCTCTGAGCTGTGAGACGTGCACCCAGAGACTGTGGCTCAACATGAGATTGCTTTC 1920
OY 1260 CTGTTGCTGGGGGGAAGCGCGATCGTGGCATCTCCGTCACCCCTCGCGGCGAGTGGGGCT 1319
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DB 1921 CTGTTGCTGGGGGGAAGCGCGATCGTGGCATCTCCGTCACCCCTCGCGGCGAGTGGGGCT 1980

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OY 1320 TGTGAACCCCAACCTGACTGAGTGGCCAGTGTGCTGCAAAATTTGGCAGAGAGTGAA 1379
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DB 1981 TGTGAACCCCAACCTGACTGAGTGGCCAGTGTGCTGCAAAATTTGGCAGAGAGTGAA 2040
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DB 2041 GGCACCTCCAAAGTGGCCAAATGATGGCAGTGTGAGCGGGGTTGCTGAGCCGTTTC 2100
OY 1440 CTGCGGGGTTCCCGCTTCCGCTTCTGTTGTTGCTTTTATGTTGTTTCAACTTATG 1499
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DB 2101 CTGCGGGGTTCCCGCTTCCGCTTCTGTTGTTGCTTTTATGTTGTTTCAACTTATG 2160
OY 1500 TTCTGCTCTGCAAGATTGTTGAGGTTTTTGTCTTCCCAAGTAGATCTGAGCAGTC 1559
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DB 2161 TTCTGCTCTGCAAGATTGTTGAGGTTTTTGTCTTCCCAAGTAGATCTGAGCAGTC 2220
OY 1560 CCCTACAGGGGTGTGGGAACAGTCAATTTTTTTTGAAGATCATTTTAACATTTATG 1619
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DB 2401 CAGTAGATATAACCCCAAGCTT 2426

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RESULT 6
US-09-060-523-3
; Sequence 3, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060, 523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660, 678
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330, 123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272, 102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32, 944
; REFERENCE/DOCKET NUMBER: 015389-000813US

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TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2426 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-060-523-3

Query Match 97.4%; Score 1719.6; DB 4; Length 2426;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Oy 1 ACCTCTAGAGAGGCTGAGACACGAAATCCCTTGAAACCCGGGAGGACAGAGTTGCAGTG 60
Db 662 ACCTACTAGAGGCTGAGACACGAAATCCCTTGAAACCCGGGAGGACAGAGTTGCAGTG 720
Oy 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCGGGAGAAAGCAAGACTCCGCTCTCA 120
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Oy 481 AAATCTTCTGTGAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGGTCTGCAGA 540
Db 1141 AAATCTTCTGTGAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGGTCTGCAGA 1200
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Oy 661 ATGGAATTTAATTTCCGCTTCCGCCCAACAGCCGCCGAGAGAGTGCATCAGAG 720
Db 1321 ATGGAATTTAATTTCCGCTTCCGCCCAACAGCCGCCGAGAGAGTGCATCAGAG 1380
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Oy 1140 GCGAGGTTGAGGCTTTTCAAGCGCGGAGGAAAGAGAGAGAGAGAGAGTCCCGCGCGGCG 1199
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Oy 1200 CCAATTCCTGAGCTGTGGAGCTGCACCCAGAGACTGGGCTCACATGCAATGCTTTC 1259
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Oy 1320 TGTGAACCCCAAACTGACTGAGTGGGCCAGTGTGCTGCAAAATTTGACAGAGACGTGA 1379
Db 1981 TGTGAACCCCAAACTGACTGAGTGGGCCAGTGTGCTGCAAAATTTGACAGAGACGTGA 2040
Oy 1380 GGCACCTCCAAAGTCGGGCAAAATGAATGGGCAATGAGCGGAGTGGCTGAGCGGCTC 1439
Db 2041 GGCACCTCCAAAGTCGGGCAAAATGAATGGGCAATGAGCGGAGTGGCTGAGCGGCTC 2100
Oy 1440 CTGGTGAGGTTCTCCGCTTCTCCGCTTTTGTGCTTATGCTTATGATTTTACACTTAA 1499
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Oy 1500 TTCCGTCTGCAAGATTTTGTGAGGTTTGTGCTTCTCCAGAGTGAATTCGACCAATC 1559
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Db 2281 AATTTTAATTAAGATTCATTAATGAACATTTGGAATTTGCTTAAATGTCATGG 2340
Oy 1680 TTTATGCCAGAGGTTGAAGTTCTTTTGAAGAAATTTAGACCTTGGCATACCTTGA 1739
Db 2341 TTTATGCCAGAGGTTGAAGTTCTTTTGAAGAAATTTAGACCTTGGCATACCTTGA 2400
Oy 1740 CAGTAGATTTAACCCTCCACAGAGCTT 1765
Db 2401 CAGTAGATTTAACCCTCCACAGAGCTT 2426

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RESULT 7  
 US-08-330-123A-3  
 Sequence 3, Application US/08330123A  
 Patent No. 5383016  
 GENERAL INFORMATION:  
 APPLICANT: VILLEPONTÉAU, Bryant  
 APPLICANT: FENG, Junli  
 APPLICANT: FUNK, Walter  
 APPLICANT: ANDREWS, William H.



```

: TITLE OF INVENTION: HUMAN TELOMERASE
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/330,123A
: FILING DATE: 27-OCT-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/272,102
: FILING DATE: 07-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 15389-000810
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2420 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-330-123A-3

Query Match      94.1%; Score 1661.2; DB 1; Length 2420;
Best local similarity 98.5%; Pred. No. 0;
Matches 1740; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

QY      1 AGCTACTCAGGAGGCTGAGACACAGAGAAATCGCTTGAACCCGGGAGGACAGAGTTGGAGTG 60
DB      662 AGCTACTCAGGAGGCTGAGACACAGAGAAATCGCTTGAACCCGGGAGGACAGAGTTGGAGTG 720
QY      61 AGCCGATCAGCGCCACTGATCCATCCAGCCTGGGGCGAAGAGCAAACTCCGCTCA 120
DB      721 AGCCGATCAGCGCCACTGATCCATCCAGCCTGGGGCGAAGAGCAAACTCCGCTCA 780
QY      121 AAAAAAATCGTTCATATTTATGGTGAATTAATCTCCCTTTTAACTCATCAAGACA 180
DB      781 AAAAAAATCGTTCATATTTATGGTGAATTAATCTCCCTTTTAACTCATCAAGACA 840
QY      181 CAGCACTACTTTAAACCAAGTCAATGATTTGAAGCCCTTCTTCTTAATAAAGGAG 240
DB      841 CAGCACTACTTTAAACCAAGTCAATGATTTGAAGCCCTTCTTCTTAATAAAGGAG 900
QY      241 ATTCACTCCTTAAGTAAATGATAGTAGTACTTCACTTGAATTAACCAATCCTCTGCTCA 300
DB      901 ATTCACTCCTTAAGTAAATGATAGTAGTACTTGAATTAACCAATCCTCTGCTCA 960
QY      301 AGGAGAAGCTGAGAGAGCAATTTCTAAGAAAAAGGGGACAGGTTGGAACTCGAGCGCATC 360
DB      961 AGGAGAAGCTGAGAGAGCAATTTCTAAGAAAAAGGGGACAGGTTGGAACTCGAGCGCATC 1020
QY      361 CCAGTGAAGCCGAGACAAAGATTCTGCTGTAGTCAAGTCTGCTGGGAATCTATTTTCACAA 420
DB      1021 CCAGTGAAGCCGAGACAAAGATTCTGCTGTAGTCAAGTCTGCTGGGAATCTATTTTCACAA 1080
QY      421 AGTTCTCAAAAAATGATGATCAAAACCTAGGAATTAAGTGTCTGTGCTTGGGCCCTA 480
DB      1081 AGTTCTCAAAAAATGATGATCAAAACCTAGGAATTAAGTGTCTGTGCTTGGGCCCTA 1140
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QY      481 AATCTCTGTGAAATTCATTTTTAAGTAGTCGAGGTGAACCCGCTGTGCTGCAGA 540
DB      1141 AATCTCTGTGAAATTCATTTTTAAGTAGTCGAGGTGAACCCGCTGTGCTGCAGA 1200
QY      541 GGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAGAGGTGCGAAG 600
DB      1201 GGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAGAGGTGCGAAG 1260
QY      601 TAAAGACGCAAGGCTTCCCGGAGGTGGGGAAGGGCAAGCTCCTTCATGGCCGGA 660
DB      1261 TAAAGACGCAAGGCTTCCCGGAGGTGGGGAAGGGCAAGCTCCTTCATGGCCGGA 1320
QY      661 ATGGAATTTAATTTCCCTTCCCAACCAAGCCGCGGAGAGAGTACTCTACAGAG 720
DB      1321 ATGGAATTTAATTTCCCTTCCCAACCAAGCCGCGGAGAGAGTACTCTACAGAG 1380
QY      721 AGCCGCGAGAGTCAGCTTGCCCAATCCGTGCGGTGCGGCGCGCTTCCTTTATAGCCGA 780
DB      1381 AGCCGCGAGAGTCAGCTTGCCCAATCCGTGCGGTGCGGCGCGCTTCCTTTATAGCCGA 1440
QY      781 CTCGCCCCGAGCGGACCGGGTTGGGAGGGTGGGCTGGAGAGGGTGGTGGCATTTT 840
DB      1441 CTCGCCCCGAGCGGACCGGGTTGGGAGGGTGGGCTGGAGAGGGTGGTGGCATTTT 1500
QY      841 TGTCTAACCTTAAGTGAAGGGCGTAGGCGCGCTTTTGTCTCCCGCGCGCTGTT 900
DB      1501 TGTCTAACCTTAAGTGAAGGGCGTAGGCGCGCTTTTGTCTCCCGCGCGCTGTT 1560
QY      901 TCTGCTGACTTTCAGCGGGCGGAAAAAGCTGCGCTGCGCGCTTCACGTTCAATTC 960
DB      1561 TCTGCTGACTTTCAGCGGGCGGAAAAAGCTGCGCTGCGCGCTTCACGTTCAATTC 1620
QY      961 GAGCAAAACAAAAATGTCAGCTGCTGCGCCCTTCCGCGCTCCGGGAGACTCGGGGGGT 1020
DB      1621 GAGCAAAACAAAAATGTCAGCTGCTGCGCCCTTCCGCGCTCCGGGAGACTCGGGGGGT 1678
QY      1021 CGCCTGCCAGCCCGCGAACCCTGAGAGCGCGGCTGGGCGCGGCGCTTCTCCGAG 1080
DB      1679 CGCCTGCCAGCCCGCGAACCCTGAGAGCGCGGCTGGGCGCGGCGCTTCTCCGAG 1737
QY      1081 GCACCTACTGCGCACCGCGAAGAGTT-GGCTCTGTCTAGCCGCGGGTCTCTGCGGGCGAAG 1139
DB      1738 GCACCCACTGCGCACCGCGAAGAGTTGGGCTGTGTACGCGCGGCTCTCTGCGGGCGAAG 1797
QY      1140 GCGAGGTTTCAAGGCTTTCAGCGCGCGGAGAAAGCAAGCAAGCAAGTCCCGCGCGGGG 1199
DB      1798 GCGAGGTTTCAAGGCTTTCAGCGCGCGGAGAAAGCAAGCAAGCAAGTCCCGCGCGGGG 1854
QY      1200 CGATTCCTGAGCTGTGGGACGTGCACCGCAGACTGGCTCACACATGCAATGCAATGCTGCTTTC 1259
DB      1855 CGATTCCTGAGCTGTGGGACGTGCACCGCAGACTGGCTCACACATGCAATGCAATGCTGCTTTC 1914
QY      1260 CTGTGTGGGGGGGGAAGCCGATGTGCGCATCCGTACCCCTGCGCGGAGTGGGGCT 1319
DB      1915 CTGTGTGGGGGGGGAAGCCGATGTGCGCATCCGTACCCCTGCGCGGAGTGGGGCT 1974
QY      1320 TGTGAACCCCAACCTGACTGACTGGGCGAGTGTCTGCAAAATTTGAGAGAGACGTGAA 1379
DB      1975 TGTGAACCCCAACCTGACTGACTGGGCGAGTGTCTGCAAAATTTGAGAGAGACGTGAA 2034
QY      1380 GGCACCTCCAAAGTCGGCCAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1439
DB      2035 GGCACCTCCAAAGTCGGCCAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2094
QY      1440 CTGCGTGGGTCTCCCGTCTCCGCTTTTGTGGCTTTTATGCTGTATTTACACTT 1499
DB      2095 CTGCGTGGGTCTCCCGTCTCCGCTTTTGTGGCTTTTATGCTGTATTTACACTT 2154
QY      1500 TTCTGCTCTGCAAGATTTTGTGAGGTTTGTCTTCCCAAGGTGATCTGACACAGTC 1559
DB      2155 TTCTGCTCTGCAAGATTTTGTGAGGTTTGTCTTCCCAAGGTGATCTGACACAGTC 2214
QY      1560 CCCTCAACGGGGGTGTGGAGAACAGTCATTTTTTTTGTGAGAGATCATTTAACATTTAATG 1619
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Db 2215 CCTCAACGGGCTGGGAGAACAGTCATTTTGTGGAGATCATTTAAACATTTAATG 2274  
Qy 1620 AATATTTAATTAAGATCTAATATGACATTTGTAATTTGTTTAAATGTCATCGG 1679  
Db 2275 AATATTTAATTAAGATCTAATATGACATTTGTAATTTGTTTAAATGTCATCGG 2334  
Qy 1680 TTTATCCAGAGGTTGAGATTTCTTTTGAATAATAGACCTTGGCATACCTTGAG 1739  
Db 2335 TTTATCCAGAGGTTGAGATTTCTTTTGAATAATAGACCTTGGCATACCTTGAG 2394  
Qy 1740 CAGTAGATATACCCCAAGCTT 1765  
Db 2395 CAGTAGATATACCCCAAGCTT 2420

RESULT 8  
US-09-580-517-3  
; Sequence 3, Application US/09580517  
; Patent No. 6320039  
; GENERAL INFORMATION:  
; APPLICANT: VILLEPONTTEAU, Bryant  
; FUNK, Walter  
; ANDREWS, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/580,517  
; FILING DATE: 25-May-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/330,123  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15389-000810  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2420 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-580-517-3

Query Match 94.1%; Score 1661.2; DB 4; Length 2420;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1740; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

Qy 1 ACCTCTCAGGAGGCTGAGACACGAAATCGTTGAACCCGAGGAGCAGAGTTGCAATG 60  
Db 662 ACCTCTCAGGAGGCTGAGACACGAAATCGTTGAACCCGAGGAGCAGAGTTGCAATG 720  
Qy 61 AGCCGAGATCAGCCACTAGACTCATCGACCTGCGGGGAGAAAGCAAGACTCCGTTCA 120

Db 721 AGCCGAGATCAGCCACTAGACTCATCGACCTGGGCGAAAGCAAGACTCCGTTCA 780  
Qy 121 AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTCTTTTACCTCATCAAGACA 180  
Db 781 AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTCTTTTACCTCATCAAGACA 840  
Qy 181 CAGCACTACTTTTAAAGCAAGTCAATGATTGAAGCCCTTCTTCTTATTAAGGAG 240  
Db 841 CAGCACTACTTTTAAAGCAAGTCAATGATTGAAGCCCTTCTTCTTATTAAGGAG 900  
Qy 241 ATTCACTCTTTAAGATTATATATATATATATATATATATATATATATATATAT 300  
Db 901 ATTCACTCTTTAAGATTATATATATATATATATATATATATATATATATATAT 960  
Qy 301 AGGAGAAGCTGGAGAGGATCTTAAGCAAAAAAGGGCGAGGTTGAACTCGAGCATC 360  
Db 961 AGGAGAAGCTGGAGAGGATCTTAAGCAAAAAAGGGCGAGGTTGAACTCGAGCATC 1020  
Qy 361 CCAGTACGCGGAGACAAAGTTCTGCTAGTCAAGTCTGCTGGGAACTATTTTCAACA 420  
Db 1021 CCAGTACGCGGAGACAAAGTTCTGCTAGTCAAGTCTGCTGGGAACTATTTTCAACA 1080  
Qy 421 AGTTCTCCAAAAATGTATATATATATATATATATATATATATATATATATAT 480  
Db 1081 AGTTCTCCAAAAATGTATATATATATATATATATATATATATATATATATAT 1140  
Qy 481 AATCTCTCTGTAATTCATTTTAAAGTATGATGATGATGATGATGATGATGATGAT 540  
Db 1141 AATCTCTCTGTAATTCATTTTAAAGTATGATGATGATGATGATGATGATGATGAT 1200  
Qy 541 GGAATGAAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTCGAG 600  
Db 1201 GGAATGAAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTCGAG 1260  
Qy 601 TAAAGACCAAAAGCCTTCCCGGAGCTGCGGAAGGCAAGCTCTCTCATATGCGCGAA 660  
Db 1261 TAAAGACCAAAAGCCTTCCCGGAGCTGCGGAAGGCAAGCTCTCTCATATGCGCGAA 1320  
Qy 661 ATGGAATTTTATTTTCCGTTCCCGCCCAACAGCCCGCGAGAGATGATCTCAAGAG 720  
Db 1321 ATGGAATTTTATTTTCCGTTCCCGCCCAACAGCCCGCGAGAGATGATCTCAAGAG 1380  
Qy 721 AGCCGAGAGTCAAGCTTGGCCATTCGGCTGGCGGCGCGCCCTCCCTTTATTAAGCCGA 780  
Db 1381 AGCCGAGAGTCAAGCTTGGCCATTCGGCTGGCGGCGCGCCCTCCCTTTATTAAGCCGA 1440  
Qy 781 CTCGCCGCGCAGCGCACCGGGTTGCGAGGAGTGGGCTGGGAGGGGTGGTGGCCATTTT 840  
Db 1441 CTCGCCGCGCAGCGCACCGGGTTGCGAGGAGTGGGCTGGGAGGGGTGGTGGCCATTTT 1500  
Qy 841 TGTCTAACCCCTAATCTGAGAGGCGTGAAGGCGGCTGTTTGTCTCCCGCGCGTGT 900  
Db 1501 TGTCTAACCCCTAATCTGAGAGGCGTGAAGGCGGCTGTTTGTCTCCCGCGCGTGT 1560  
Qy 901 TCTCGCTGACTTTCAAGGCGGAGAAAGCCTCGGCTGGCGGCTTCAACCTTCAATTCTA 960  
Db 1561 TCTCGCTGACTTTCAAGGCGGAGAAAGCCTCGGCTGGCGGCTTCAACCTTCAATTCTA 1620  
Qy 961 GAGCAAAACAAAATATGACAGTCTGTGGCCGTTTCCCGCGGAGACTTGGCGGAGT 1020  
Db 1621 GAGCAAAACAAAATATGACAGTCTGTGGCCGTTTCCCGCGGAGACTTGGCGGAGT 1678  
Qy 1021 CGCGTCCGACGCCCGCAACCCGCGCTGAGAGCGCGGCTGGCGGCGGCTTCTCGGAG 1080  
Db 1679 CGCGTCCGACGCCCGCAACCCGCGCTGAGAGCGCGGCTGGCGGCGGCTTCTCGGAG 1737  
Qy 1081 GCACCTACTGCAACCGCGCAAGATT- GGGTCTGTCAAGCGCGGAGTCTTCTCGGAGGAG 1139  
Db 1738 GCACCTACTGCAACCGCGCAAGATTGAGGCTGTGTCAAGCGCGGAGTCTTCTCGGAGGAG 1797  
Qy 1140 GCGAGGTTTCAAGCTTTTCAAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199  
Db 1798 GCGAGGTTTCAAGCTTTTCAAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1854

OY 1200 CGATTCCCTGAGCTGTGGGAGCGTGAACCCAGACCTGGGCTCACACATGACGTTGCTTTC 1259  
DB 1855 CGATTCCCTGAGCTGTGGGAGCGTGAACCCAGACCTGGGCTCACACATGACGTTGCTTTC 1914  
OY 1260 CTGTTGGTGGGGGGAACGCCGATCGTGGCAGTCGTCACCCCTCGCCGGCAGTGGGGCT 1319  
DB 1915 CTGTTGGTGGGGGGAACGCCGATCGTGGCAGTCGTCACCCCTCGCCGGCAGTGGGGCT 1974  
OY 1320 TGTGAACCCCAAACTGACTGACTGGGCCAGTGTCTGCAAAATGGCAGAGAGCTGAA 1379  
DB 1975 TGTGAACCCCAAACTGACTGACTGGGCCAGTGTCTGCAAAATGGCAGAGAGCTGAA 2034  
OY 1380 GGCACCTCCAAAGTGGGCAAAATGATGGGAGTGGGAGCGGGGCTGCTGGAGCGCTTC 1439  
DB 2035 GGCACCTCCAAAGTGGGCAAAATGATGGGAGTGGGAGCGGGGCTGCTGGAGCGCTTC 2094  
OY 1440 CTGCGTGGGCTTCCGCTCTCCGCTTTTGTGCTTTTATGTTGATTTACACTTAG 1499  
DB 2095 CTGCGTGGGCTTCCGCTCTCCGCTTTTGTGCTTTTATGTTGATTTACACTTAG 2154  
OY 1500 TTCTCTCTGCGAGATTTTGTGAGGTTTGTCTTCCCAAGGTAGATCTGACAGCTC 1559  
DB 2155 TTCTCTCTGCGAGATTTTGTGAGGTTTGTCTTCCCAAGGTAGATCTGACAGCTC 2214  
OY 1560 CCCTCAACGGGCTGTGGGAGAACGTCATTTTGTGAGAGATCATTTAATTAATG 1619  
DB 2215 CCCTCAACGGGCTGTGGGAGAACGTCATTTTGTGAGAGATCATTTAATTAATG 2274  
OY 1620 AATATTTAATTAAGATCTAATTAATGAACATTTGTTCTTTAATGCTATCG 1679  
DB 2275 AATATTTAATTAAGATCTAATTAATGAACATTTGTTCTTTAATGCTATCG 2334  
OY 1680 TTATATCCGAGAGTTTGAAGTTCTTTTGAAGAAATTAAGACCTTGGCGATGACTTGA 1739  
DB 2335 TTATATCCGAGAGTTTGAAGTTCTTTTGAAGAAATTAAGACCTTGGCGATGACTTGA 2394  
OY 1740 CAGTAGATTAACCCCAACAGCTT 1765  
DB 2395 CAGTAGATTAACCCCAACAGCTT 2420

RESULT 9  
US-08-485-778-1  
Sequence 1, Application US/08485778  
Patent No. 5876979  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel Athena  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Greider, Carol  
APPLICANT: Marheine, Maria Antonia Blasco  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,778  
FILING DATE: 07-JE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2425 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-485-778-1  
Query Match  
Best Local Similarity 98.4%; Score 1640.8; DB 2; Length 2425;  
Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8:  
OY 1 AGCTACTCAGGAGGCTGAGACAGAGAAATCGTTGAACCGGGAGGACAGGTTGACATG 60  
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OY 181 CAGCAGTACTTTAAACCAAAATGATTAAGCAAGCGCTTTCTTCTTAATAAAGGAG 240  
DB 841 CAGCAGTACTTTAAACCAAAATGATTAAGCAAGCGCTTTCTTCTTAATAAAGGAG 900  
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OY 301 AGGAGAGCTGGAGAGGCAATCTTAAGGAGAAAGGGGCAAGGCTTGGAACTCGGACGATC 360  
DB 961 AGGAGAGCTGGAGAGGCAATCTTAAGGAGAAAGGGGCAAGGCTTGGAACTCGGACGATC 1020  
OY 361 CCATGAGCCGAGACAAAGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 1021 CCATGAGCCGAGACAAAGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
OY 421 AGTTTCACAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
DB 1081 AGTTTCACAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
OY 481 AATCTTCCGTGAATTCATTTTAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
DB 1141 AATCTTCCGTGAATTCATTTTAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
OY 541 GATAGAAAAAGGCGCTGATACCTCAAGTTAGTTTACCTTTAAGAGGAGGAGGAGGAGGAG 600  
DB 1201 GATAGAAAAAGGCGCTGATACCTCAAGTTAGTTTACCTTTAAGAGGAGGAGGAGGAGGAG 1260  
OY 601 TAAAGAGCAAGCCCTTCCCGGAGCTGGGAGAGGAGCAAGCTCTTCTCATGCGCGGAA 660  
DB 1261 TAAAGAGCAAGCCCTTCCCGGAGCTGGGAGAGGAGCAAGCTCTTCTCATGCGCGGAA 1320  
OY 661 ATGGAATTTAATTTCCCGTTCCCGCAACCAAGCCCGCGGAGAGAGTACTCAGAG 720

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Db 1321 ATGGAATTTATTTCCCGTTCCCGCCAAACGACCGCCGAGAGAGTCTTCACAGAG 1380  
QY 721 AGCGCGAGAGTCAAGCTTGGSCAATCCGTGGCGTGGGGCCGCTCCCTTTATAGCCGA 780  
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QY 957 TCTAGAGCAAAACAAAAATGTCAGCTGTGCGCCCTTCGCGCGCTCGCGCGCGCTTCGC 1016  
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Db 1680 GGTGCG-CTGCTTCGC 1737  
QY 1077 GGAAGCACTACTACTGCGCGCGAGAGATT- GGTCTGTGCGCGCGCGCGCGCGCGCGCGCG 1135  
Db 1738 GGAAGCACTACTACTGCGCGCGAGAGATT- GGTCTGTGCGCGCGCGCGCGCGCGCGCGCG 1797  
QY 1136 GAGGGCGAGTTTCAAGCGCTTTCAGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1195  
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QY 1196 GGGCGAGTTTCCGTGAGAGTGTGGAGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1255  
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Db 1976 GCGTTGTGAACCCCAACCTGACTGAGTGGCGAGTGTGCTCAAAATTGGCAGGAGAGC 2035  
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Db 2036 TGAAGGACACTCCAAAGTGGGCAAAATGAATGAGCGGGGGTGGCTGGAGCC 2095  
QY 1436 GTTTCGTCGCTGGGTTCTCCGCTTTCGCGTTTGTGCTTTATGTTGATTTACAC 1495  
Db 2096 GTTTCGTCGCTGGGTTCTCCGCTTTCGCGTTTGTGCTTTATGTTGATTTACAC 2155  
QY 1496 TTTAGTTCCTGCTTGCAGATTTTGTGAGGTTTGTCTCTCCCAAGGATGATCTCGACC 1555  
Db 2156 TTTAGTTCCTGCTTGCAGATTTTGTGAGGTTTGTCTCTCCCAAGGATGATCTCGACC 2215  
QY 1556 AGTCCCTCAACGCGGGTGGGAGACAGTCAATTTTGTGAGAGATGATTTACATTT 1615  
Db 2216 AGTCCCTCAACGCGGGTGGGAGACAGTCAATTTTGTGAGAGATGATTTACATTT 2275  
QY 1616 AATGAATATTTAATTAAGAGATCTAATGAGATGGAATTTGTGCTTTAATGATG 1675  
Db 2276 AATGAATATTTAATTAAGAGATCTAATGAGATGGAATTTGTGCTTTAATGATG 2335  
QY 1676 TCGGTTTATGCGAGAGAGTGAAGTTTCTTTTGAAGAAATTAAGACCTTGGGATGACT 1735  
Db 2336 TCGGTTTATGCGAGAGAGTGAAGTTTCTTTTGAAGAAATTAAGACCTTGGGATGACT 2395  
QY 1736 TGAGCAGTAGATATTAACCCCAAGCTT 1765  
|||||

Db 2396 TGAGCAGTAGATATTAACCCCAAGCTT 2425  
RESULT 10  
US-08-520-550A-1  
; Sequence 1, Application US/08520550A  
; Patent No. 6013468  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Avillion, Ariel A.  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Greider, Carol  
; APPLICANT: Marhuenda, Maria A. B.  
; APPLICANT: Villeneuve, Bryant  
; TITLE OF INVENTION: RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,550A  
; FILING DATE: 29-AUG-1995  
CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/387,524  
; FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-9540  
; TELEFAX: 617-861-6240  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-520-550A-1  
Query Match 93.0%, Score 1640.8, DB 3, Length 2425;  
Best Local Similarity 98.4%, Pred. No. 0;  
Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8;  
QY 1 AGCTACTCAGAGGCTGAGACAGAGATTCCTTGAACCCCGGAGGAGAGCTTGCAGTG 60  
Db 602 AGCTACTCAGAGGCTGAGACAGAGATTCCTTGAACCCCGGAG- GAGAGGTTGCAGTG 720  
QY 61 AGCGGAGATCAAGCGCATAGACTCATTCACAGCTGGGGGAGAGAGCAAGAGCTCCGTCA 120  
Db 721 AGCGGAGATCAAGCGCATAGACTCATTCACAGCTGGGGGAGAGAGCAAGAGCTCCGTCA 780  
QY 121 AAAAAAAAAATCGTTACATTTATGTTGATTTACTCCCTCTCTTTTACCTCATCAAGACA 180  
Db 781 AAAAAAAAAATCGTTACATTTATGTTGATTTACTCCCTCTCTTTTACCTCATCAAGACA 840

OY 181 CAGCACTACTTTAAAGCAAGTCAATGATTGAAGCCCTTTCTTCTTAATAAAAGGAG 240  
 DB 841 CAGCACTACTTTAAAGCAAGTCAATGATTGAAGCCCTTTCTTCTTAATAAAAGGAG 900  
 OY 241 ATTCACTCTTAAGATTAAATAGTAGTACACTTGAATTAAGCCATCTCTCTCA 300  
 DB 901 ATTCACTCTTAAGATTAAATAGTAGTACACTTGAATTAAGCCATCTCTCTCA 960  
 OY 301 AGGAGAACTGGAGAAAGCATTTCTAAGGAAAAAGGGGCAAGGTTGAACTCGAGCCATC 360  
 DB 961 AGGAGAACTGGAGAAAGCATTTCTAAGGAAAAAGGGGCAAGGTTGAACTCGAGCCATC 1020  
 OY 361 CCACTGAGCCGAGACAAAGATTGCTGTAGTCAAGTCTGCTGGGAAATCTATTTCACAA 420  
 DB 1021 CCACTGAGCCGAGACAAAGATTGCTGTAGTCAAGTCTGCTGGGAAATCTATTTCACAA 1080  
 OY 421 AGTTCTCAAAAAATGTGATGATCAAAACTAGGAATTAAGTGTCTGTCTTAAGCCCTA 480  
 DB 1081 AGTTCTCAAAAAATGTGATGATCAAAACTAGGAATTAAGTGTCTGTCTTAAGCCCTA 1140  
 OY 481 AATCTCTCTGTGATTTTCAATTTTAAAGTAGTCCGAGGTGAACCCGCTGTCTGACAA 540  
 DB 1141 AATCTCTCTGTGATTTTCAATTTTAAAGTAGTCCGAGGTGAACCCGCTGTCTGACAA 1200  
 OY 541 GGATGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAGAAAGGTGGGAAG 600  
 DB 1201 GGATGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAGAAAGGTGGGAAG 1260  
 OY 601 TAAAGACGCAAAAGCCCTTTCGCGAGCTGGCGAAAGGCAAGTCTCTCATGAGCGGAA 660  
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 OY 661 ATGGAATCTTAATTTTCCCTTCCCTCCCAACCAAGCCCGCCGAGAGTAGTCTACGAG 720  
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 DB 1381 ACCCGGAGAGTACAGCTTGGCCAAATCCGTGGGGGCGGCTCTTTAATTAAGCCGA 1440  
 OY 781 CTCGCGCCGCGACGCGACCGGGTTC---GGAAGGTGGGCTGGGAAGGGGTGGCCAT 836  
 DB 1441 CTCGCGCCGCGACGCGACCGGGTTC---GGAAGGTGGGCTGGGAAGGGGTGGCCAT 1500  
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 DB 1501 TTTTCTCTTAACCTTAAGTGAAGAGGGGCTAGGCGCGTCTTCTCTCCGCGCGCTG 1560  
 OY 897 TTTTCTCTCTGACTTTTCAAGCGGGGGAAGGCTGCGGCTGCGGCTTCAACCGTTCA 956  
 DB 1561 TTTTCTCTCTGACTTTTCAAGCGGGGGAAGGCTGCGGCTGCGGCTTCAACCGTTCA 1620  
 OY 957 TCTAGAGCAAAACAAATGTGAGTGTGCGCCGTTTCGCCCTCCCGGGGAACTTGGGC 1016  
 DB 1621 TCTAGAGCAAAACAAATGTGAGTGTGCGCCGTTTCGCCCTCCCGGGGAACTTGGGC 1679  
 OY 1017 GGGTGGCTGGCCGAGCCCGGAAACCCGCTGAGGCGCGGCTGGCGCGGGGCTTCTCC 1076  
 DB 1680 GGGTGGCTGGCCGAGCCCGGAAACCCGCTGAGGCGCGGCTGGCGCGGGGCTTCTCC 1737  
 OY 1077 GGAGGCACTTACTGCGACCGCGGAAGATT--GGCTCTGTAGCGGGGGGTCTCGGGGGGC 1135  
 DB 1738 GGAGGCACTTACTGCGACCGCGGAAGATT--GGCTCTGTAGCGGGGGGTCTCGGGGGGC 1797  
 OY 1136 GAGGCGGAGTTTCAGGCTTTTCAGGCGCGAGGAAGAGAGGAGGAGTCTCCCGCGGC 1195  
 DB 1798 GAGGCGGAGTTTCAGGCTTTTCAGGCGCGAGGAAGAGAGGAGGAGTCTCCCGCGGC 1855  
 OY 1196 GCGCGGATTCCTGAGCTGTGGAGCTGCAACGAGAGTCTGCGCTCACATGCAAGTTCCG 1255  
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OY 1256 TTTCTGTGTGGGAGGGAACGCCGATCGGCGCATCCGACCCCTCGCGGAGTGGG 1315  
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 OY 1316 GGGTTTGAACCCCAACCTGACTGAGTGGGCACTGTCTGCAAAATTGGCAGGAGAG 1375  
 DB 1976 GGGTTTGAACCCCAACCTGACTGAGTGGGCACTGTCTGCAAAATTGGCAGGAGAG 2035  
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 OY 1436 GTTCTGCGGTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTATTAACAC 1495  
 DB 2096 GTTCTGCGGTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTATTAACAC 2155  
 OY 1496 TTAGTCTGCTGTGAGATTTTGTGAGGTTTTCCTTCCCAAGTAGATCTGAGC 1555  
 DB 2156 TTAGTCTGCTGTGAGATTTTGTGAGGTTTTCCTTCCCAAGTAGATCTGAGC 2215  
 OY 1556 AGTCCCTCAAGGGGTGTGGGAGAACAGTCAATTTTGTGAGAGATCAATTAATTT 1615  
 DB 2216 AGTCCCTCAAGGGGTGTGGGAGAACAGTCAATTTTGTGAGAGATCAATTAATTT 2275  
 OY 1616 AATGAATATTTAATTAAGAGATCTAATAGACATTTGGAATGTCTTAAATGCTCA 1675  
 DB 2276 AATGAATATTTAATTAAGAGATCTAATAGACATTTGGAATGTCTTAAATGCTCA 2335  
 OY 1676 TCGGTTATGCCAGAGGTTAGAAATTTCTTTTGAATAATAGACCTTGGGATGACT 1735  
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 DB 2396 TGAGCAGTAGATATTAACCCCAACAGCTT 2425

RESULT 11  
 US-08-714-482-2  
 ; Sequence 2, Application US/08714482  
 ; Patent No. 5972605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Halley, Calvin  
 ; APPLICANT: Halley, Calvin  
 ; TITLE OF INVENTION: Assays for Regulators of Mammalian  
 ; TITLE OF INVENTION: Telomerase Expression  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/714,482  
 ; FILING DATE: 16-SEP-1996  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/521,634  
 ; FILING DATE: 31-AUG-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/482,115  
 ; FILING DATE: 07-JUN-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/472,802  
 ; FILING DATE: 07-JUN-1995  
 ; PRIORITY APPLICATION DATA:

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: APPLICATION NUMBER: US 08/330,123
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/272,102
: FILING DATE: 07-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-00860US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 981 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: -
: LOCATION: 1..981
: OTHER INFORMATION: /note="PstI fragment containing htr
: OTHER INFORMATION: sequence"
: US-08-714-482-2

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Query Match      54.8%; Score 967.4; DB 2; Length 981;
Best Local Similarity 99.8%; Pred. No. 1.7e-271;
Matches 979; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 534 CTGCAGAGTATGAAAAAAGGCCCTTGATACCTCAAGTTAGTTACCTTTAAGAAG 593
DB 1 CTGCAGAGTATGAAAAAAGGCCCTTGATACCTCAAGTTAGTTACCTTTAAGAAG 60
QY 594 TCGGAGTAAAGACGAAACCTTTCCCGAGCTGGGAGGAGGCAAGCTTTCCATG 653
DB 61 TCGGAGTAAAGACGAAACCTTTCCCGAGCTGGGAGGAGGCAAGCTTTCCATG 120
QY 654 GCCGGAATGAACCTTAAATTTCCCGTTCGCCCAACAGCCCGCCGAGAGTACTC 713
DB 121 GCCGGAATGAACCTTAAATTTCCCGTTCGCCCAACAGCCCGCCGAGAGTACTC 180
QY 714 TCACGAGACCGGAGAGTACGTTGGCCAATCCGTGGGCGGCTCCCTTTAT 773
DB 181 TCACGAGACCGGAGAGTACGTTGGCCAATCCGTGGGCGGCTCCCTTTAT 240
QY 774 AAGCCGACTGCGCCGACGACCGGCTTGGCGAGGCTGGGCTGGAGGGGTGGTGC 833
DB 241 AAGCCGACTGCGCCGACGACCGGCTTGGCGAGGCTGGGCTGGAGGGGTGGTGC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGAGGCGTAGGCGCGCTTTTCTCCCGCGC 893
DB 301 CATTTTGTCTAACCTTAAGTGAAGAGGCGTAGGCGCGCTTTTCTCCCGCGC 360
QY 894 CTGTTTCTGCTGACTTTCAGCGGCGGAAAGCGCTGCGCGCTTCCACCGTT 953
DB 361 CTGTTTCTGCTGACTTTCAGCGGCGGAAAGCGCTGCGCGCTTCCACCGTT 420
QY 954 CATTTAGAGCAAAATAATGTAGCTGTGGCCGCTTCCCGCTCCCGGGGACCTGC 1013
DB 421 CATTTAGAGCAAAATAATGTAGCTGTGGCCGCTTCCCGCTCCCGGGGACCTGC 480
QY 1014 GCGGGGTGCGCCCGCCAGCCCGGAAACCCGCTGAGGCGCGGCTCGCCGGGCTTC 1073
DB 481 GCGGGGTGCGCCCGCCAGCCCGGAAACCCGCTGAGGCGCGGCTCGCCGGGCTTC 540
QY 1074 TCCGAGAGCACTTACTGCGACCGCAAGAGTT-GGCTGTGTAGCGCGGCTCTCGGG 1132
DB 541 TCCGAGAGCACTTACTGCGACCGCAAGAGTTGGCTGTGTAGCGCGGCTCTCGGG 600
QY 1133 GCGGAGGCGGAGCTTACGCTTTAGGCGCGAGAGAGAGAGAGAGTCCCGCG 1192
DB 601 GCGGAGGCGGAGCTTACGCTTTAGGCGCGAGAGAGAGAGAGAGTCCCGCG 660

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QY 1193 GCGGAGGCGGATTCCTGAGCTGTGGAGCTGACCCAGAGACTGCGCTACACATCACTT 1252
DB 661 GCGGAGGCGGATTCCTGAGCTGTGGAGCTGACCCAGAGACTGCGCTACACATCACTT 720
QY 1253 CGCTTCCGTGTGTGGGGAAGCCCGATCGTGGCATCTGCAACCCCTGCGGGCAGT 1312
DB 721 CGCTTCCGTGTGTGGGGAAGCCCGATCGTGGCATCTGCAACCCCTGCGGGCAGT 780
QY 1313 GGGGGCTTGTGAACCCCAACCTGACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGAG 1372
DB 781 GGGGGCTTGTGAACCCCAACCTGACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGAG 840
QY 1373 ACCTGAGGCACTCCAAAGTGGCCAAATGAATGGGAGAGAGCCGGGCTGCTGGA 1432
DB 841 ACCTGAGGCACTCCAAAGTGGCCAAATGAATGGGAGAGAGCCGGGCTGCTGGA 900
QY 1433 GCGGTTCCTGCTGGGTTCTCCCGTCTTCCGCTTTTGTGCTTTATGTTGATATAC 1492
DB 901 GCGGTTCCTGCTGGGTTCTCCCGTCTTCCGCTTTTGTGCTTTATGTTGATATAC 960
QY 1493 AACTTAGTTCTGCTGCTGAG 1513
DB 961 AACTTAGTTCTGCTGCTGAG 981

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RESULT 12
US-08-710-249-5
: Sequence 5, Application US/08710249
: Patent No. 5858777
: GENERAL INFORMATION:
: APPLICANT: Villeponteau, Bryant
: APPLICANT: Feng, Junli
: APPLICANT: Andrews, William H.
: APPLICANT: Adams, Robert R.
: TITLE OF INVENTION: Methods and Reagents for Regulating
: TITLE OF INVENTION: Telomere Length and Telomerase Activity
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/710,249
: FILING DATE: 13-SEP-1996
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/583,808
: FILING DATE: 05-JAN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/003,492
: FILING DATE: 08-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-001220US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 981 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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OY	534	CTGCAGAGAAATGAAAAAGCCCTCGATATCCCTCAAGTTAGTTACCTTTAAAGAG	593
Db	1	CTGCAGAGAGATAGAAAAAGACCCTCTGATACCTCAAGTTAGTTACCTTTAAAGAG	60
OY	594	TCGGAAGTAAAGACCAAAAGCTTTCCCGAGCTGCGGAAGGGCAACGTCTCTCATG	653
Db	61	TCGGAAGTAAAGACCAAAAGCTTTCCCGAGCTGCGGAAGGGCAACGTCTCTCATG	120
OY	654	GCCGGAATGGAACCTTAATTTCCCGTTCCCGCCCAACACCGCCCGCCGAGAGTACATC	713
Db	121	GCCGGAATGGAACCTTAATTTCCCGTTCCCGCCCAACACCGCCCGCCGAGAGTACATC	180
OY	714	TCACAGAGACCCGCGAGAGTCAGCTTGGCCAAATCCGTGCGGTGCGAGCGCGCTCCCTTAAT	773
Db	181	TCACAGAGACCCGCGAGAGTCAGCTTGGCCAAATCCGTGCGGTGCGAGCGCGCTCCCTTAAT	240
OY	774	AAGCGACTCGCCCGGACGCGACCCGGGTTGCGAAGGATGGGCTGGGAGAGGGTGGTGAC	833
Db	241	AAGCGACTCGCCCGGACGCGACCCGGGTTGCGAAGGATGGGCTGGGAGAGGGTGGTGAC	300
OY	834	CATTTTGTGTAAACCCCTAACTGAGAAAGGGCGTAAGCGCGCTCTTTGGTCTCCCGCGG	893
Db	301	CATTTTGTGTAAACCCCTAACTGAGAAAGGGCGTAAGCGCGCTCTTTGGTCTCCCGCGG	360
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OY	954	CATTCTAGAGCAAAACAAAAATGTCACTGCTGCGCCCTTGCCGCTCCCGGGAGACTGC	1011
Db	421	CATTCTAGAGCAAAACAAAAATGTCACTGCTGCGCCCTTGCCGCTCCCGGGAGACTGC	480
OY	1014	GCGCGGTGCGCTGGCCGACGCCCGGCAACCCCGGCTGAGAGGGCGGGGTCGCGCGGGCTTC	107
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OY	1074	TCGCGAGGCACTACTGCGACCCCGGAAGAGTT--GGCTGTGACAGCGGGGCTCTCGGG	1133
Db	541	TCGCGAGGCACTACTGCGACCCGGAAGAGTGGGGCTCTGACAGCCGGGGTCTCTCGGG	600
OY	1133	GCGGAGGGCGAGGTTCAAGGCTTTCAGGGCGGAGAGAGGAACGAGAGTCCCGCGG	1199
Db	601	GCGGAGGGCGAGGTTCAAGGCTTTCAGGGCGGAGAGAGGAACGAGAGTCCCGCGG	660
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OY	1253	GCGTTTCTGTGGTGGGGGGGAACGGCGATGTCGCGCATTCGCTACCCCTCGCGGCAAT	1311
Db	721	GCGTTTCTGTGGTGGGGGGGAACGGCGATGTCGCGCATTCGCTACCCCTCGCGGCAAT	780
OY	1313	GGGGGCTGTGTAACCCCAAACTGACTGAGCTGGGCGCAGTGTCTGCAAAATTGGACGAG	1373
Db	781	GGGGGCTGTGTAACCCCAAACTGACTGAGCTGGGCGCAGTGTCTGCAAAATTGGACGAG	840
OY	1373	ACGTGAAGGCACTCCCAAAAGTCGGCCAAATGAAATGGGACGTACGCCGGGTTGCTTGA	1433
Db	841	ACGTGAAGGCACTCCCAAAAGTCGGCCAAATGAAATGGGACGTACGCCGGGTTGCTTGA	900
OY	1433	GCGGTCCTGCGTGGGTTCTCCGCTTCCGCTTTTGTGTTGATGTTATGTTATGTTATAC	1493
Db	901	GCGGTCCTGCGTGGGTTCTCCGCTTCCGCTTTTGTGTTGATGTTATGTTATGTTATAC	960
OY	1493	AACCTAATGCTCTGCTGTCGAG 1513	
Db	961	AACCTAATGCTCTGCTGTCGAG 981	

RESULT 14  
US-08-770-565-1  
; Sequence 1, Application US/08770565  
; Patent No. 5846723

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: GENERAL INFORMATION:
: APPLICANT: Kim, Nam Woo
: APPLICANT: Wu, Fred
: APPLICANT: Kealey, James T.
: APPLICANT: Pruzan, Ronald
: APPLICANT: Weinlich, Scott L.
: TITLE OF INVENTION: Methods for Detecting the RNA Component of
: TITLE OF INVENTION: Telomerase
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/770,565
: FILING DATE: 20-DEC-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-002300US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 981 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: OS-08-770-565-1

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Query Match	54.7%	Score 965.8 ; DB 2 ;	Length 981 ;
Best Local Similarity	99.7% ;	Pred. No. 5e-271 ;	
Matches 978 ;	Conservative 0 ;	Mismatches 2 ;	Indels 1 ;
			Gaps 1 ;
QY 534 CTGCAGAGATAGAAAAAAGGCGCTCTCATATCCCTCAAGTTAGTTACACCTTTAAAGAAAG 593			
Db 1 CTGCAGAGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTACACCTTTAAAGAAAG 60			
QY 594 TCGGAAGTAAAGACGCCAAGCCTTTCGCCGAGTGTCCGAAAGGACAGCTCTTCTCATATG 653			
Db 61 TCGGAAGTAAAGACGCCAAGCCTTTCGCCGAGCTGTCCGAAAGGACAGCTCTTCTCATATG 120			
QY 654 GCCGGAATGTGAACCTTATATTCCTCGTTCCCGCCCAACAGCCCGCCGAGAGAGATGC 713			
Db 121 GCCGGAATGTGAACCTTATATTCCTCGTTCCCGCCCAACAGCCCGCCGAGAGAGATGC 180			
QY 714 TCACAGAGACCCGCGAGATCAGCTTGGCCAAATCCGTGCGGTGCGGCGCGCTCCCTTTAT 773			
Db 181 TCACAGAGACCCGCGAGATCAGCTTGGCCAAATCCGTGCGGTGCGGCGCGCTCCCTTTAT 240			
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QY 834 CATTTTGTGTAAACCTCACTGAGAAAGGGGTAGGACCTGTGCTTTTGTCTCCCGCGCG 893			
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QY 894 CTGTTTTCCTGCGTACTTTACGGGGGCGGAAAGACCTGTGCGCTGTGCGGCTTTCACAGCTT 953			
Db 361 CTGTTTTCCTGCGTACTTTACGGGGGCGGAAAGACCTGTGCGCTGTGCGGCTTTCACAGCTT 420			



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OY 954 CATCTAGAGCAAAACAAAATGTGAGCTGTGCCCCGTTCCGCCCGGAGACTTC 1013
DB 421 CATCTAGAGCAAAACAAAATGTGAGCTGTGCCCCGTTCCGCCCGGAGACTTC 480
OY 1014 GCGGGGTGCGCTGCGCCAGCCCGGAAACCCCGCTGAGAGCGCGGCTTC 1073
DB 481 GCGGGGTGCGCTGCGCCAGCCCGGAAACCCCGCTGAGAGCGCGGCTTC 540
OY 1074 TCCGAGGACCTACTGACCGACCGCAAGAGTT-GGCTGTGTAGCGCGGCTTC 1132
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DB 601 GCGGAGGCGAGCTTCAGCGCTTCAGCGCGCAAGAGAGAGAGAGAGAGAG 660
OY 1193 GCGGCGGCGATTCCTGAGCTGTGGAGCTGCAACCGAGACTCGGCTCAGAT 1252
DB 661 GCGGCGGCGATTCCTGAGCTGTGGAGCTGCAACCGAGACTCGGCTCAGAT 720
OY 1253 GCGTTTCCTGTGTGTGGGGGAAAGCGCATGTGGCATCGCTACCCCTGCG 1312
DB 721 GCGTTTCCTGTGTGTGGGGGAAAGCGCATGTGGCATCGCTACCCCTGCG 780
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OY 1433 GCGGTTCCGTGCGTGGGGTTCGCGCTTCCTGCTTTTGTGCTTTTATGAT 1492
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OY 1493 AACTAGTTCCTGCTGTGAG 1513
DB 961 AACTAGTTCCTGCTGTGAG 981

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RESULT 15
US-08-833-377-1
: Sequence 1, Application US/08833377
: Patent No. 5968506
: GENERAL INFORMATION:
: APPLICANT: Weinlich, Scott L.
: APPLICANT: Atkinson III, Edward M.
: APPLICANT: Lichtenstein, Serge P.
: APPLICANT: Vasserot, Alain P.
: APPLICANT: Pruzan, Ronald A.
: APPLICANT: Kealey, James T.
: TITLE OF INVENTION: Purified Telomerase
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/833,377
: FILING DATE: 04-APR-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/510,736
: FILING DATE: 04-AUG-1995

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: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: TELEPHONE/DOCKET NUMBER: 015389-001110US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 981 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY:
: LOCATION: 1..981
: OTHER INFORMATION:
: OTHER INFORMATION: Sautiral-HindIII fragment of clone 28-1"
US-08-833-377-1

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Query Match 54.7% Score 965.8: DB 2: Length 981:
Best Local Similarity 99.7%: Pred. No. 5e-271:
Matches 978: Conservative 0: Mismatches 2: Indels 1: Gaps 1:

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 Job time : 120 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 69 seconds  
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Title: US-09-601-267-1

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1719.6	97.4	2426	10 US-09-057-351-3	Sequence 3, Appl1
2	883.4	50.1	4118	10 US-09-068-821-17	Sequence 17, Appl1
3	881.6	49.9	962	10 US-09-018-125-1	Sequence 1, Appl1
4	881.6	49.9	962	10 US-09-068-821-16	Sequence 16, Appl1
5	841.6	47.7	975	10 US-09-068-821-20	Sequence 20, Appl1
6	835.4	47.3	4118	10 US-09-068-821-18	Sequence 18, Appl1
7	835.2	47.3	975	10 US-09-068-821-21	Sequence 21, Appl1
8	830.4	47.0	975	10 US-09-068-821-19	Sequence 19, Appl1
9	546.4	31.0	560	10 US-09-057-351-1	Sequence 1, Appl1
10	101.8	5.8	180216	10 US-09-835-232-6	Sequence 6, Appl1
11	101.2	5.7	32193	10 US-09-764-877-2623	Sequence 2623, Ap
12	101.2	5.7	684973	10 US-09-263-959-1	Sequence 1, Appl1
13	99.6	5.6	302250	10 US-09-962-832-154	Sequence 154, Ap
14	99.6	5.6	9914	10 US-09-764-847-1558	Sequence 1558, Ap
15	99	5.6	31994	9 US-09-764-904-71	Sequence 71, Appl1
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17	98.6	5.6	28897	10 US-09-764-877-3897	Sequence 3897, Ap
18	98	5.6	289	10 US-09-764-877-2732	Sequence 2732, App
19	97.6	5.5	2756	10 US-09-764-853-898	Sequence 898, App

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c 24	96.4	5.5	32193	10 US-09-764-847-1549	Sequence 1549, Ap
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c 45	94.8	5.4	32195	10 US-09-764-870-617	Sequence 617, App

#### ALIGNMENTS

RESULT 1  
US-09-057-351-3  
Sequence 3, Application US/09057351  
Patent No. US20010034439A1  
GENERAL INFORMATION:  
APPLICANT: Valleepteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2426 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-057-351-3

Query Match 97.4%; Score 1719.6; DB 10; Length 2426;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Patent No. US2002012969A1  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Method of quantifying tumour  
TITLE OF INVENTION: cells in a body fluid and a suitable test kit  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain

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STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PADAT Sequenzmodul Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068.821
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 42 795.5
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 7249-1501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-068-821-17
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Query Match          50.1%; Score 883.4; DB 10; Length 4118;
Best Local Similarity 97.6%; Pred. No. 1.1e-222;
Matches 950; Conservative 0; Mismatches 16; Indels 7; Gaps 5;

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DB 968 CCCCCACAAGCTT 980
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RESULT 3
US-09-018-125-1
; Sequence 1, Application US/09018125A
; Patent No. US20010007902A1
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Kondo, Seiji
; APPLICANT: Cowell, John K.
; APPLICANT: Li, Guiyang
; APPLICANT: Torrence, Paul F.
; TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
; TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES
; FILE REFERENCE: 8656-022
; CURRENT APPLICATION NUMBER: US/09/018,125A
; CURRENT FILING DATE: 1999-02-03
; EARLIER APPLICATION NUMBER: 60/044,507
; EARLIER FILING DATE: 1997-04-21
; NUMBER OF SEO ID NOS: 9
; SOFTWARE: Patentln Ver. 2.0
; SEO ID NO 1
; LENGTH: 962
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-018-125-1
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Query Match          49.9%; Score 881.6; DB 10; Length 962;
Best Local Similarity 73.5%; Pred. No. 1.6e-222;
Matches 711; Conservative 236; Mismatches 14; Indels 7; Gaps 5;

QY 799 GGGTTGCGAGGCTGAGGCTGGGAGGCGGTGCGCCATTTTGTCTAACCTTACTGAG 858
   |||
DB 1 GGGUUGCGGAGGUGGCGCUGGAGGCGUGGCGCAUUUUUUUUUUUUAACCUAAGUGAG 60
   |||
QY 859 AAGGCGGTAGGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTTACGG 918
   |||
DB 61 AAGGCGGUAAGGCGCGCUGUUUUUUGCUCGCCGCGCGUGUUUUUUCUGCGUACUUUCAGCG 120
   |||
QY 919 GGGGGAAGAGCCTCGGCTGCGCGCTTCCACCGTTCTATCTAGAGCAAAACAAATGTC 978
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DB 121 GGGGGAAGAGCCTCGGCTGCGCGCGCUCUCCAGCUUUCACCGUUUCUAGAGCAAAACAAAUUUGC 180
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QY 979 AGCTGCTGCCCCGCTTCCGCCCTCCGGGAGACCTGCGCGGGGCTGCGCCACGCCCCGA 1038
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Db 181 AGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 238
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1039 ACCCGCGCTGGAGGCGCGCGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1098
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 239 ACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 297
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1099 AAGAGTT-GGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1157
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 298 AAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 356
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1158 AGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1217
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 357 AGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1218 GAGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1277
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 415 GAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
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QY 1278 CCGATCGTGGCGAGTCCGTCACCCCTCGCGGCGGAGTGGGGGCTGTGAACCCGCAACCTG 1337
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 475 CCGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
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QY 1338 ACTGACTGGGCGAGTGTGTGCAAAATTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1397
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Db 535 ACUGACUGGCGGAGUGUGUGCAAAUUGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
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QY 1398 CAAATGAATGGGCGAGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1457
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 595 CAAATGAATGGGCGAGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 654
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QY 1458 CTTCGCGCTTTTGTGCTTGTGTTATGTTATACAACTAGTCTGCTGCTGCTGCTGCTG 1517
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Db 655 CTTCGCGCTTTTGTGCTTGTGTTATGTTATACAACTAGTCTGCTGCTGCTGCTGCTG 714
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QY 1518 TGTGAGAGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1577
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Db 715 TGTGAGAGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 774
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1578 AGAAGAGTATTTTGTGAGAGATCATTTATGATTTATGATTTATGATTTATGATTTATG 1637
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 775 AGAAGAGTATTTTGTGAGAGATCATTTATGATTTATGATTTATGATTTATGATTTATG 834
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QY 1638 CTAAATGAACATTTGAAATTTGTTCTTAAATGTCATCGGTTTATGTCAGAGAGTTAGA 1697
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 835 CTAAATGAACATTTGAAATTTGTTCTTAAATGTCATCGGTTTATGTCAGAGAGTTAGA 894
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1698 AGTTTCTTTTGAATAATTAAGACCTTGGCGATGACCTTGGAGAGAGATTAACCCCG 1757
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 895 AGTTTCTTTTGAATAATTAAGACCTTGGCGATGACCTTGGAGAGAGATTAACCCCG 954
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1758 ACAAGCTT 1765
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 955 ACAAGCTT 962
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PADAT sequenzmodul Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,821
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 42 795.5
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 7249-1501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO.: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 962 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-068-821-16

Query Match          49.9%; Score 881.6; DB 10; Length 962;
Best Local Similarity 97.8%; Pred. No. 1.6e-222;
Matches 947; Conservative 0; Mismatches 14; Indels 7; Gaps 5;

QY 799 GGGTGGCGGAGGGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 858
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 GGGTGGCGGAGGGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 859 AAGGCGGTAGGCGCGCGCTGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 918
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AAGGCGGTAGGCGCGCGCTGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 120
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QY 919 GCGGGAAGAAAGCTCGGCGCTGCGCGCTTGCACCGCTTATCTAGAGCAAAAGAAATGTC 978
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GCGGGAAGAAAGCTCGGCGCTGCGCGCTTGCACCGCTTATCTAGAGCAAAAGAAATGTC 180
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QY 979 AGCTGCTGCGCGCTTGCACCGCTTGCACCGCTTGCACCGCTTGCACCGCTTGCACCGCTTGC 1038
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Db 181 AGCTGCTGCGCGCTTGCACCGCTTGCACCGCTTGCACCGCTTGCACCGCTTGCACCGCTTGC 238
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QY 1039 ACCCGCGCTGAGAGCGCGGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1098
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Db 239 ACCCGCGCTGAGAGCGCGGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 297
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QY 1099 AAGAGTT-GGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1157
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Db 298 AAGAGTTGGGCTGTGTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 356
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QY 1158 AGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1217
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Db 357 AGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
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QY 1218 GAGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1277
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 415 GAGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1278 CCGATCGTGGCGAGTCCGTCACCCCTCGCGGCGGAGTGGGGGCTGTGAACCCGCAACCTG 1337
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 475 CCGATCGTGGCGAGTCCGTCACCCCTCGCGGCGGAGTGGGGGCTGTGAACCCGCAACCTG 534
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1338 ACTGACTGGGCGAGTGTGTGCAAAATTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1397
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Db 535 ACTGACTGGGCGAGTGTGTGCAAAATTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1398 CAAATGAATGGGCGAGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1457
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Db 595 CAAATGATGCGAGTACCGCGGGTTCCTGAGCCGTTCCCTGCGTTCCTCCGT 654  
QY 1458 CTTCCGCTTTTGTGCTTTTATGTTATTAACAATTAGTTCGTCTGCAGATT 1517  
Db 655 CTTCCGCTTTTGTGCTTTTATGTTATTAACAATTAGTTCGTCTGCAGATT 714  
QY 1518 TGTGAGGTTTGTCTCTCCCAAGGTAGATCTCGACAGTCCCTCAAGGGGTGGG 1577  
Db 715 TGTGAGGTTTGTCTCTCCCAAGGTAGATCTCGACAGTCCCTCAAGGGGTGGG 774  
QY 1578 AGAAGATCTTTTGTGAGATCATTTAATGATTTAATTAATTAAGAAT 1637  
Db 775 AGAAGATCTTTTGTGAGATCATTTAATGATTTAATTAATTAAGAAT 834  
QY 1638 CTAATGACATTTGTAATGTCTTAAATGATCGTGTATGACAGGTTAGA 1697  
Db 835 CTAATGACATTTGTAATGTCTTAAATGATCGTGTATGACAGGTTAGA 894  
QY 1698 AGTTCTTTTGTGAAAAATTAAGACCTTGGCATGACCTTGGAGAGTATTAACCCC 1757  
Db 895 AGTTCTTTTGTGAAAAATTAAGACCTTGGCATGACCTTGGAGAGTATTAACCCC 954  
QY 1758 ACAAGCTT 1765  
Db 955 ACAAGCTT 962

RESULT 5  
US-09-068-821-20  
; Sequence 20, Application US/09068821  
; Patent No. US20020012969A1  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Method of quantifying tumour  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McElain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PADAT Sequenzmodul Version 1.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/068,821  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 195 42 795.5  
; FILING DATE: 16-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; TELEPHONE: (619)238-0062  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ. ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 975 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic RNA  
; US-09-068-821-20

Query Match 47.7%; Score 841.6; DB 10; Length 975;  
Best local similarity 71.3%; Pred. No. 5.3e-212;  
Matches 690; Conservative 232; Mismatches 39; Indels 7; Gaps 5;

QY 794 GCACCGGTTGCGAGAGGTGGCCCTGGAGAGGGGAGGCCATTATTTTGTCTAACCCTAA 853  
Db 14 GCGCGGGGUGCGGAGAGGUGGCGCUGGAGAGGGUGGCGCAUUUUUUUUUAUCCUAA 73  
QY 854 CTGAGAGGGCGTAGGCGCCGTCTTGTCTCCCGCGCCGTCTTGTCTGCTGACTTT 913  
Db 74 CUGAGAGGGCGTAGGCGCCGTCTTGTCTCCCGCGCCGTCTTGTCTGCTGACTTT 133  
QY 914 CAGCGGGCGGAAAAACCTCGGCTGCCCTTCCACCTGTTCTTAGAGCAAAACAAA 973  
Db 134 CAGCGGGCGGAAAAACCTCGGCTGCCCTTCCACCTGTTCTTAGAGCAAAACAAA 193  
QY 974 ATGTCAGCTGCTGGCCGCTTGGCCGCTTGGGAGACCTGGGCGGGGCTGCTGCCAGCC 1033  
Db 194 AUGTCAGCTGCTGGCCGCTTGGCCGCTTGGGAGACCTGGGCGGGGCTGCTGCCAGCC 251  
QY 1034 CCGGAACCCCGCTGAGAGCGCGGCTGGCCCGGCGGCTTCCGAGAGCACTACTGCCA 1093  
Db 252 CCGGAACCCCGCTGAGAGCGCGGCTGGCCCGGCGGCTTCCGAGAGCACTACTGCCA 310  
QY 1094 CCGGGAAGATT--GCTCTGTCAAGCGCGGGGTCTCTGCGGGCGAGGGCGAGTTCAAGC 1152  
Db 311 CCGGGAAGAGUUGGGGCUUCUCAAGCCGCGGUCUCUGGGGGGAGGGCGAGGUCU--CC 369  
QY 1153 CTTTCAGGCGCGAGAGAGAGAGGAGGAGTCCCGCGCGGGGCGGAGTTCCTGAGC 1212  
Db 370 GDUUCAGGCGCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 427  
QY 1213 TGTGAGAGCTGACCCAGAGAGCTGCGGCTGACATGACATGACATGACATGACATGACATG 1272  
Db 428 UUGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 487  
QY 1273 GAAGCGGATGCTGCGGATCGCTGACCCCTGCGCGGCGGAGTGGAGGCCCTTGAACCCCAA 1332  
Db 488 GAAGCGGATGCTGCGGATCGCTGACCCCTGCGCGGCGGAGTGGAGGCCCTTGAACCCCAA 547  
QY 1333 ACCTGACGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1392  
Db 548 ACCUGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 607  
QY 1393 TCGGCGCAATGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1452  
Db 608 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 667  
QY 1453 CCGGCTTCCGCTTTTGTGCTTTTATGTTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1512  
Db 668 CCGGCTTCCGCTTTTGTGCTTTTATGTTATTAAGTATTAAGTATTAAGTATTAAGTATTA 727  
QY 1513 GATTTGTGAGGTTTGTGCTTTTATGTTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1572  
Db 728 GAUU 787  
QY 1573 GTGAGAGACAGTCAATTTTGTGAGAGATCAATTAATTAATTAATTAATTAATTAATTA 1632  
Db 788 UGGGAGAGACAGTCAATTTTGTGAGAGATCAATTAATTAATTAATTAATTAATTAATTA 847  
QY 1633 AAGATCTAATGAACATTTGATGTTCTTTAATGTTCTGATGTTCTGATGTTCTGATGTTCT 1692  
Db 848 AAGATCTAATGAACATTTGATGTTCTTTAATGTTCTGATGTTCTGATGTTCTGATGTTCT 907  
QY 1693 TTAGAGATTTCTTTTGAAGAAATTAAGCTTGGCGATGACCTTGAAGCAATAGATTA 1752  
Db 908 UUGAAGUU 967  
QY 1753 CCCCCACA 1760  
Db 968 CCCCCACA 975

RESULT 6  
US-09-068-821-18  
; Sequence 18, Application US/09068821

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: Patent No. US20020012969A1
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Method of quantifying tumour
: TITLE OF INVENTION: cells in a body fluid and a suitable test kit
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PADAT Sequenzmodul Version 1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/068,821
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 195 42 795.5
: FILING DATE: 16-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 7249-1501
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ. ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4118 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: US-09-068-821-18

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Query Match      47.3%; Score 835.4; DB 10; Length 4118;
Best Local Similarity 94.6%; Pred. No. 4.7e-210;
Matches 920; Conservative 0; Mismatches 46; Indels 7; Gaps 5;

QY 794 GCACCGGCTTGGCGAGGCTGGGCTGGAGGCGTGGCCATTTTGTCTAACCTTAA 853
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DB 14 GCGCGGGCTTGGCGAGGCTGGGCTGGAGGCGTGGCCATTTTGTCTAACCTTAA 73

QY 854 CTGAGAGGCGCTAGGCGGCTTGTCTTCCCGGCGGCTTTTCTCGCTGACTTT 913
   |||||||
DB 74 CTGAGAGGCGCTAGGCGGCTTGTCTTCCCGGCGGCTTTTCTCGCTGACTTT 133

QY 914 CACGCGGCGGAAAAGCGCTGCGCTTCCCGGCTTCCACCGTTTCTAGAGCAAAACAAA 973
   |||||||
DB 134 CACGCGGCGGAAAAGCGCTGCGCTTCCCGGCTTCCACCGTTTCTAGAGCAAAACAAA 193

QY 974 ATCTCAGCTGCTGGCGGCTTCCCGGCTTCCCGGCTTCCCGGCTTCCCGGCTTCC 1033
   |||||||
DB 194 ATCTCAGCTGCTGGCGGCTTCCCGGCTTCCCGGCTTCCCGGCTTCCCGGCTTCC 251

QY 1034 CCGGAGCGCGCTGGAGGCGGCGGCTTCCCGGCTTCCCGGAGCAACCTACCTGCA 1093
   |||||||
DB 252 CCGGAGCGCGCTGGAGGCGGCGGCTTCCCGGAGCAACCTACCTGCA 310

QY 1094 CCGCGAAGATT-GGCTCTGTCTAGCCGCGGCTTCTCGGGGCGAGGCGAGGTTAGGC 1152
   |||||||
DB 311 CCGCGAAGATTGGGCTGTGTAGCGCGGCGGCTTCTCGGGGCGAGGCGAGGTTAA-CC 369

QY 1153 CTTCGAGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
   |||||||
DB 370 GTTTCAGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427

QY 1213 TGTGGAGAGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272

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DB 428 TGTGGAGAGCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487

QY 1273 GAACCGGAGATGCGGAGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1332
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DB 488 GAACCGGAGATGCGGAGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 547

QY 1333 ACCTGAGTACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1392
   |||||||
DB 548 ACCTGAGTACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607

QY 1393 TCGGCGCAAAATGAATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1452
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DB 608 CTGTGTACATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667

QY 1453 CCGGCTCTCCGCTTTTGTGCTTCTTATGCTGTATTAACATTTAGTCTCTGCA 1512
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DB 668 CCGGCTCTCCGCTTTTGTGCTTCTTATGCTGTATTAACATTTAGTCTCTGCA 727

QY 1513 GATTTGTAGGTTTGTGCTTCTTCCAGAGTATGATGATGATGATGATGATGATGAT 1572
   |||||||
DB 728 GATTTGTAGGTTTGTGCTTCTTCCAGAGTATGATGATGATGATGATGATGATGAT 787

QY 1573 GTGGGAGAGAGATGATTTTGTGAGAGATGATTTAATTTAATTTAATTTAATTTAG 1632
   |||||||
DB 788 GTGGGAGAGAGATGATTTTGTGAGAGATGATTTAATTTAATTTAATTTAATTTAG 847

QY 1633 AAGATCTAAATGAACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1692
   |||||||
DB 848 AAGATCTAAATGAACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 907

QY 1693 TTGAGATTTCTTTTGTGAAAATTTAGACCTTGGCGATGACCTTGGAGATGATATA 1752
   |||||||
DB 908 TTGAGATTTCTTTTGTGAAAATTTAGACCTTGGCGATGACCTTGGAGATGATATA 967

QY 1753 CCCCCACAGCTT 1765
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DB 968 CCCCCACAGCTT 980

```

```

RESULT 7
US-09-068-821-21
: Sequence 21, Application US/09068821
: Patent No. US20020012969A1
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Method of quantifying tumour
: TITLE OF INVENTION: cells in a body fluid and a suitable test kit
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PADAT Sequenzmodul Version 1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/068,821
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 195 42 795.5
: FILING DATE: 16-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 7249-1501
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999

```



TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 975 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic RNA  
 US-09-068-821-21

Query Match 47.3%; Score 835.2; DB 10; Length 975;  
 Best Local Similarity 71.0%; Pred. No. 2,6e-210;  
 Matches 687; Conservative 231; Mismatches 43; Indels 7; Gaps 5;

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QY 794 GCACCGGTTGCGGAGGTTGGCTGGAGGGTGTGGCATTTTGTGCTAACCTTAA 853
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 GCGCGGGGUGGCGGAGGUGGCGGUGGAGGUGGUGGCAUUUUUUGCUAACCUAA 73
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 854 CTGAGAAAGGCGTAGGCGCGCTTTGCTCCCGCGCGCTTTTTCGCTGACTTT 913
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 CUGAGAAAGGCGTAGGCGCGCTTTGCTCCCGCGCGCTTTTTCGCTGACTTT 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 914 CACGGGGCGGAAAGCCTGCGCTGCGCTTCCACCGTTTCATTCTAGACAAACAAA 973
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 CACGGGGCGGAAAGCCTGCGCTGCGCTTCCACCGTTTCATTCTAGACAAACAAA 193
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 974 ATGTACAGCTGTGCGCCCTTCCCGGGGACCTGGGGGGTGGCTGCTCCAGCC 1033
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 194 AUGUCAGGUCUGGCGCCGUGC--CCUCCCGGGGACCGGCGGUGGUGGUGCCAGCC 251
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1034 CCGCAACCCCGCTGAGAGCGCGGTCGCGCGGCTTCTCCGAGAGCACTACTGCA 1093
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 252 CCGCAACCCCGCTGAGAGCGCGGTCGCGCGGCTTCTCCGAGAGCACTACTGCA 310
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1094 CCGCGAAGATT-GGCTGTGTACCGCGCGGCTCTCGGGGGGAGGCGAGGTTCA 1152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 311 CCGCGAAGATTGGGCGUCUCUACCGCGGCGUCUCUGGGGGGAGGCGAGGTTCA 369
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1153 CTTTCAGCGCGGAGAAAGAGAGAGAGAGTCCCGCGCGGCGCGGCTTCCCTGAGC 1212
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 370 GGUUCAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
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QY 1213 TGTGGAGAGTGCACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 428 UUGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1273 GAAGCGCGAGTGTGCGAGATCCGTACCCCTCGCGGCGAGTGGGGGCTGTGAACCCCA 1332
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 488 GAAGCGCGAGTGTGCGAGATCCGTACCCCTCGCGGCGAGTGGGGGCTGTGAACCCCA 547
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1333 ACCTGACTGACTGGGCGAGTGTGCTCAATTTGGCAGAGAGAGAGAGAGAGAGAG 1392
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 548 ACCUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1393 TCGGCGCAAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1452
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 608 CUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
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QY 1453 CCGGCTTCGCTTTTGTGCTTTTATGTTGATTTACACTTATGTTCTGCTGCA 1512
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 668 CCGGCTTCGCTTTTGTGCTTTTATGTTGATTTACACTTATGTTCTGCTGCA 727
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1513 GATTGTGAGGTTTGTGCTTCCCAAGTAGACTGTGACAGAGTCCCTCAAGGGGT 1572
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 728 GAUUUUUGUGUGUUUUUGUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 787
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1573 GTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1632
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 788 UGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1633 AGATCTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 848 AAGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 907
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```

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QY 1693 TTGAGAGTTCTTTTGGAAATAGACCTTGGCATGACCTTGAGCAGTAGATATA 1752
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Db 908 UUGAGAGUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 967
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1753 CCCCCACA 1760
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 968 CCCCCACA 975
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

## RESULT 8

US-09-068-821-19  
 Sequence 19, Application US/09068821  
 Patent No. US20020012969A1

## GENERAL INFORMATION:

APPLICANT:  
 TITLE OF INVENTION: Method of quantifying tumour  
 TITLE OF INVENTION: cells in a body fluid and a suitable test kit  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PADAT sequenzmodul Version 1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/068,821  
 FILING DATE:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 42 795.5  
 FILING DATE: 16-NOV-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 7249-1501  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999

## INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 975 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic RNA  
 US-09-068-821-19

## Query Match

Best Local Similarity 70.7%; Score 830.4; DB 10; Length 975;  
 Matches 684; Conservative 231; Mismatches 46; Indels 7; Gaps 5;

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QY 794 GCACCGGTTGCGGAGGTTGGCTGGAGGGTGTGGCATTTTGTGCTAACCTTAA 853
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Db 14 GCGCGGGGUGGCGGAGGUGGCGGUGGAGGUGGUGGCAUUUUUUGCUAACCUAA 73
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 854 CTGAGAAAGGCGTAGGCGCGCTTTGCTCCCGCGCGCTTTTTCGCTGACTTT 913
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 CUGAGAAAGGCGTAGGCGCGCTTTGCTCCCGCGCGCTTTTTCGCTGACTTT 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 914 CACGGGGCGGAAAGCCTGCGCTGCGCTTCCACCGTTTCATTCTAGACAAACAAA 973
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 CACGGGGCGGAAAGCCTGCGCTGCGCTTCCACCGTTTCATTCTAGACAAACAAA 193
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 974 ATGTACAGCTGTGCGCCCTTCCCGGGGACCTGGGGGGTGGCTGCTCCAGCC 1033
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 194 AUGUCAGGUCUGGCGCCGUGC--CCUCCCGGGGACCGGCGGUGGUGGUGCCAGCC 251
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```

[illegible]

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: PatentIn Release #1.0, Version #1.30
4
5  CURRENT APPLICATION DATA:
6  APPLICATION NUMBER: US/09/057,351
7  FILING DATE: 08-APR-1994
8  CLASSIFICATION: 435
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/272,102
11 FILING DATE: 07-JUL-1994
12
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/330,123
15 FILING DATE: 27-OCT-1994
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/472,802
19 FILING DATE: 07-JUN-1995
20
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Storella, John R.
23 REGISTRATION NUMBER: 32,944
24 REFERENCE/DOCKET NUMBER: 015389-000821US
25
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (415) 576-0200
28 TELEFAX: (415) 576-0500
29
30 INFORMATION FOR SEQ ID NO: 1:
31 SEQUENCE CHARACTERISTICS:
32     LENGTH: 560 base pairs
33     TYPE: nucleic acid
34     STRANDEDNESS: single
35     TOPOLOGY: linear
36
37 MOLECULE TYPE: RNA (genomic)
38
39 US-09-057-351-1

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[illegible]

DB 541 ACUGACUGGCGCAGUGUCU 560

## RESULT 10

US-09-835-232-6/c  
; Sequence 6, Application US/09835232  
; Patent No. US20020098489A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leder, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/09/835,232  
; PRIORITY FILING DATE: 2001-04-12  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 180216  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(180216)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-835-232-6

Query Match 5.8%; Score 101.8; DB 10; Length 180216;  
Best Local Similarity 88.5%; Pred. No. 4,4e-16;

Matches 123; Conservative 0; Mismatches 12; Indels 4; Gaps 1;

QY 1 AGCTACTCAGGAGCTGAGACAGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

DB 64485 AGCTACTCAGGAGCTGAGAGGAGAGAAATGTTGAACCCGGAGGAGGAGTTGCAGTG 64426

QY 61 AGCGGAGATCGGCGCTACATCTCCAGCGCTGGCGGAAAGAGCAAGCTCCGTCTCA 120

DB 64425 AGCGGAGATCGGCGCTACATCTCCAGCGCTGGCGGAAAGAGCAAGCTCCGTCTCA 64370

QY 121 AAAAAAAAAATCTTACAA 139

DB 64369 AAAAAAAAAAATTATA 64351

## RESULT 11

US-09-764-877-2623/c  
; Sequence 2623, Application US/09764877  
; Patent No. US20020147140A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005  
; CURRENT APPLICATION NUMBER: US/09/764,877  
; PRIORITY FILING DATE: 2001-01-17  
; PRIOR APPLICATION data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2623  
; LENGTH: 32193  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-2623

Query Match 5.7%; Score 101.2; DB 10; Length 32193;  
Best Local Similarity 86.2%; Pred. No. 2.7e-16;

Matches 112; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGCTGAGACAGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

DB 31984 AGCTACTCAGGAGCTGAGAGGAGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 31925

QY 61 AGCGGAGATCGGCGCTACATCTCCAGCGCTGGCGGAAAGAGCAAGCTCCGTCTCA 120

DB 31924 AGCTACTCAGGAGCTGAGAGGAGAGAAATGTTGAACCCGGAGGAGGAGTTGCAGTG 31865

QY 121 AAAAAAAAAA 130

DB 31864 AAAAAAAAAA 31855

## RESULT 12

US-09-263-959-1/c  
; Sequence 1, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 05-MAR-1999  
; APPLICATION NUMBER: US/09/263,959  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 684973 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: Linear  
US-09-263-959-1

Query Match 5.7%; Score 101.2; DB 10; Length 684973;  
Best Local Similarity 86.2%; Pred. No. 1.2e-15;

Matches 112; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGCTGAGACAGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

DB 442801 AGCTACTCAGGAGCTGAGAGGAGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 442742

QY 61 AGCGGAGATCGGCGCTACATCTCCAGCGCTGGCGGAAAGAGCAAGCTCCGTCTCA 120

DB 442741 AGCGGAGATCGGCGCTACATCTCCAGCGCTGGCGGAAAGAGCAAGCTCCGTCTCA 442682

QY 121 AAAAAAAAAA 130

DB 442681 AAAAAAAAAA 442672

## RESULT 13

US-09-962-832-154/c  
; Sequence 154, Application US/09962832  
; Patent No. US20020110821A1  
; GENERAL INFORMATION:

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; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154
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Query Match
Best Local Similarity 5.6%; Score 99.6; DB 10; Length 302250;
Matches 111; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAAACCCGGGAGGAGAGTTGCAGTG 60
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Db 226482 AGCTACTCGGAGGCTGAGGAGAGAAATCGCTTGAAACCCGGGAGGAGGCTGCGGTG 226423

QY 61 AGCCGAGATCAGCGCCACTAGACTTCATCCAGCCTGGCGGAAAGAGCAAGACTCCGCTCA 120
    |||||||
Db 226422 AGCCGAGATCAGCGCCACTGTAATCTGACAGAGCCGCGGCGAGAGCAAGCACTCATCTCA 226363

QY 121 AAAAAAAAAA 130
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Db 226362 AAAAAAACA 226353
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RESULT 14
US-09-764-847-1558/c
; Sequence 1558, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1558
; LENGTH: 9914
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1558
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Query Match
Best Local Similarity 5.6%; Score 99.2; DB 10; Length 9914;
Matches 133; Conservative 0; Mismatches 33; Indels 4; Gaps 1;
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QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAAACCCGGGAGGAGAGTTGCAGTG 60
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QY 61 AGCCGAGATCAGCGCCACTAGACTTCATCCAGCCTGGCGGAAAGAGCAAGACTCCGCTCA 120
    |||||||
Db 8377 AGCCGAGATGTCACACTGCACCT---CAGCCTGGGTGACAGAGCAAGACTCTGTCTCA 8322

QY 121 AAAAAAAAAATGTTACATTTATGGTGGATTACTCCCTCTTTTAACTT 170
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Db 8321 AAAAAAAAAATGTTTATTTTATTAATAGCCAGGCTGCTGTCAT 8272
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RESULT 15
US-09-764-904-71/c
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; Sequence 71, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764,904
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 71
; LENGTH: 31994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-904-71
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```
Query Match
Best Local Similarity 5.6%; Score 99; DB 9; Length 31994;
Matches 114; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAAACCCGGGAGGAGAGTTGCAGTG 60
    |||||||
Db 5801 AGTTACTTGGAGGCTGAGAGAGAAATCGCTTGAACTGGAGGAGGAGTTGCAGTG 5742

QY 61 AGCCGAGATCAGCGCCACTAGACTTCATCCAGCCTGGCGGAAAGAGCAAGACTCCGCTCA 120
    |||||||
Db 5741 AGCCGAGATGCGACCATTCGACCCAGCCAGCCTGGCGCAACAGAGCAAGCATATGCTCA 5682

QY 121 AAAAAAAAAATCGTTACA 139
    |||||
Db 5681 AAAAAAACA 5663
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Search completed: December 19, 2002, 15:13:48
Job time : 1612 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 2130 Seconds  
(without alignments)  
13420.204 Million cell updates/sec

Title: US-09-601-267-1

Perfect score: 1765  
Sequence: 1 agctactcagagagctgaga.....gataataccccacacagctt 1765

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estcda:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estcov:\*  
6: em\_estcpl:\*  
7: em\_estcro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_hum:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rpod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	424.2	24.0	443	9	AI825849 tdl9d01.x
c 2	390.8	22.1	421	10	AM293800 UT-H-B12-
c 3	371.4	21.0	412	10	AM136367 UT-H-B11-
c 4	355.4	20.1	376	9	AI180754 tlf97g05.x
c 5	355.2	20.1	388	10	AM207347 UI-H-B11-
c 6	351.4	19.9	353	14	BM695101 UI-E-CL1-BM695101

Result No.	Score	Query Match	Length	ID	Description
c 7	110.8	6.3	466	17	AQ229478 HS-2021_A
c 8	109.2	6.2	680	17	AG186502 Pan tTrog1
c 9	107.6	6.1	418	17	AQ390169 CITR1-E1-
c 10	107.2	6.1	469	13	BM509394 h117f10.y
c 11	107.2	6.1	516	13	B1468297 1d87b01.y
c 12	107.2	6.1	529	14	BQ270800 1K05b06.y
c 13	107.2	6.1	556	14	BQ267333 1K02c03.y
c 14	107.2	6.1	589	14	BQ270346 1K09g10.y
c 15	106.4	6.0	635	17	AQ428429 CITR1-E1-
c 16	106	6.0	774	17	AQ751486 HS-3576-B
c 17	104.8	5.9	671	17	AQ418931 RPT-11-1
c 18	104.6	5.9	465	17	AQ527107 CITR1-E1-
c 19	104.6	5.9	815	14	BQ429052 AGENCOURT
c 20	104.4	5.9	303	14	BM672404 UI-E-CQ0-
c 21	104.4	5.9	712	17	AG139751 Pan tTrog1
c 22	103.8	5.9	451	14	N66929 za47h09.s1
c 23	103	5.8	837	13	B1820230 603037070
c 24	103	5.8	1074	14	BQ429712 AGENCOURT
c 25	102.8	5.8	318	13	B1492686 dE27908.w
c 26	102.8	5.8	340	10	AM021747 dE27908.y
c 27	102.8	5.8	684	17	AG109444 Pan tTrog1
c 28	102	5.8	364	17	AQ333390 HS-5010_A
c 29	101.6	5.8	256	9	AA084337 zn04b05.s
c 30	101.2	5.7	382	10	AV764523 AV764523
c 31	101.2	5.7	474	9	A1866580 t251c10.x
c 32	101.2	5.7	514	17	B37536 HS-1044-A1-
c 33	101.2	5.7	735	9	AU120382 AU120382
c 34	101.2	5.7	773	12	B6221771 RST41586
c 35	101.2	5.7	815	12	BF382750 60181513
c 36	101.2	5.7	859	17	AQ750588 HS-5573_B
c 37	101.2	5.7	925	12	BG249993 602362061
c 38	101	5.7	445	17	AQ198078 RPT11-46
c 39	100.4	5.7	504	9	AI138096 DKFZP547B
c 40	100.2	5.7	335	9	AA492202 hg78e08.s
c 41	100	5.7	459	17	AQ483064 RPT-11-2
c 42	99.8	5.7	404	14	W07861 zB04q03.r1
c 43	99.8	5.7	460	9	AI597733 tu91a08.x
c 44	99.8	5.7	464	10	AW150226 x949d01.x
c 45	99.8	5.7	662	17	AQ262070 CITR1-E1-

#### ALIGNMENTS

RESULT 1  
AI825849/c 443 bp mRNA linear EST 24-AUG-1999  
tdl9d01.x1 NCI\_CGAP\_Col6 Homo sapiens cDNA clone IMAGE:2076097 3',  
LOCUS  
DEFINITION  
RNA sequence.  
ACCESSION  
AI825849  
VERSION  
AI825849.1 GI:5446520  
KEYWORDS  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 443)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
Contact: Robert Strassberg, Ph.D.  
COMMENT  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
, Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

#### FEATURES

```

source
1..443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2076097"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Col6 was
prepared, and 85 circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      78 a      144 c      151 g      68 t      2 others
ORIGIN
Query Match      24.0%; Score 424.2; DB 9; Length 443;
Best Local Similarity 98.6%; Pred. No. 1.7e-94;
Matches 437; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 895 TGTTCCTTCGCTGACTTTCAGCGGGGGGAGAAAGCCTCGCGCCCTTCACCGTTTC 954
DB 443 TGTTCCTTCGCTGACTTTCAGCGGGGGGAGAAAGCCTCGCGCCCTTCACCGTTTC 384
QY 955 ATTCTAGAGCAAAACAAAATGTACGCTGCGCCCTTCGCGCCCTTCGCGGGACCTGCG 1014
DB 383 ATTCTAGAGCAAAACAAAATGTACGCTGCGCCCTTCGCGCCCTTCGCGGGACCTGCG 324
QY 1015 GCGGCTCGCTGCGCCAGCCCGCCGAGGAGCGCGGCTGCGCCCGGGGCTTCT 1074
DB 323 GCGGCTCGCTGCGCCAGCCCGCCGAGGAGCGCGGCTGCGCCCGGGGCTTCT 264
QY 1075 CCGGAGGCACTACTGCGACCGCGGAGAGTT-GGCTGTGTACGCGGAGTCTCTCGGGG 1133
DB 263 CCGGAGGCACTACTGCGACCGCGGAGAGTTGGCTGTGTACGCGGAGTCTCTCGGGG 204
QY 1134 GCGAGGGGAGGTTGAGGCTTTCAGGCGCGGAGGAGGAGGAGGAGGAGTCCCCGGG 1193
DB 203 GCGAGGGGAGGTTGAGGCTTTCAGGCGCGGAGGAGGAGGAGGAGGAGTCCCCGGG 144
QY 1194 GCGGAGGCACTTCCCTGAGCTGTGAGCTGACCCAGGACTCGGCTCACACATGAGTTTC 1253
DB 143 GCGGAGGCACTTCCCTGAGCTGTGAGCTGACCCAGGACTCGGCTCACACATGAGTTTC 84
QY 1254 GCTTTCCTGTTGGTGGGGGAGACCGCATTCGTGCCATTCGTCACCCCTCGCGGCACTG 1313
DB 83 GCTTTCCTGTTGGTGGGGGAGACCGCATTCGTGCCATTCGTCACCCCTCGCGGCACTG 24
QY 1314 GGGGCTGTGAACCCCAAACT 1336
DB 23 GGGGCTGTGAACCCCAAACT 1

```

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RESULT 2
AM293800/c      421 bp      mRNA      linear      EST 16-JAN-2000
LOCUS           IMAGE:2727679 3, mRNA sequence.
DEFINITION      UT-H-BI2-ahp-f-04-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
ACCESSION       AM293800
VERSION         AM293800.1 GI:6700436
KEYWORDS        EST.
SOURCE          human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 421)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL        Tumor Gene Index
                Unpublished (1997)

```

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COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILN at:
www.bio.lnl.gov/dbtrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 197-273,
>GC rich#low-complexity
Seq primer: M13 Forward
POLYA=yes.

```

#### FEATURES

##### SOURCE

```

Location/Qualifiers
1..421
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2727679"
/clone_lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. B1 constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Col10, NCI_CGAP_Col16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CuL1,
NCI_CGAP_Le12, NCI_CGAP_Br23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_Gc4, NCI_CGAP_Gc6,
NCI_CGAP_Br25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1: LLM 3334-3337, 3682-3683,
3798-3803 (IMAGE cloneids 132376-132381),
145608-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1:
LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE cloneids
1323912-1325831, 1471368-1472903, 1492104-1493255)
NCI_CGAP_Lu5 pool 1: LLM 3575-3582, 3851-3854 (IMAGE
cloneids 1414920-1417991, 1520904-1522439) NCI_CGAP_Gc4
pool 1: LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE
cloneids 1257096-1258631, 1465064-1470983, 1475592-1476743
) NCI_CGAP_Pr22 pool 1: LLM 2457-2459, 2758-2759,
3062-3068 (IMAGE cloneids 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Col1 pool 1: LLM 2644-2653,
2871-2872 (IMAGE cloneids 1057416-1061255, 1144584-1145351
) Subtraction was performed as previously described
(Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.].
TAG_LIB=NCI_CGAP_Col10
TAG_TISSUE=colon
TAG_SEQ=AAACG"

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BASE COUNT      68 a      135 c      143 g      75 t
ORIGIN
Query Match      22.1%; Score 390.8; DB 10; Length 421;
Best Local Similarity 99.3%; Pred. No. 3.2e-86;
Matches 403; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 846 AACCTAAGTGAAGGCGGAGGCGGCTTTGCTCCCGCGCGCTTTTCTCG 905
DB 421 ACCCTAAGTGAAGGCGGAGGCGGCTTTGCTCCCGCGCGCTTTTCTCG 362
QY 906 CTGACTTTACGGGGGAGAAAGCTCGGCTCGCGCTTCACCGTTCTAGAGCA 965
DB 361 CTGACTTTACGGGGGAGAAAGCTCGGCTCGCGCTTCACCGTTCTAGAGCA 302
QY 966 AACAAAATGTACGTGCGCCGTTGCGCCCTCCCGGGAGCTCGCGGCGGCT 1025

```

|||||  
 Db 301 AACAAAAATGTAGCTGTGCGCCGCTCCCTCCCGGAGCATGCGCGGCT 242  
 QY 1026 GCCACGCCCCGAAACCCCGCTGAGAGCCGCGGCTCGCGGCTTCTCCGAGGCACC 1085  
 Db 241 GCGGACCCCCGAAACCCCGCTGAGAGCCGCGGCTCGCGGCTTCTCCGAGGCACC 182  
 QY 1086 TACTGCACCGCAAGAGTT-GGCTCTGTTCAGCGCGGCTCTCTCGGAGCGAGGGCGAG 1144  
 Db 181 CACTGCGACCGCAAGAGTTGGGCTCTGTTCAGCGCGGCTCTCTCGGAGCGAGGGCGAG 122  
 QY 1145 GTTCAGGCTTTGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1204  
 Db 121 GTTCAGGCTTTGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62  
 QY 1205 CCTGAGCTGTGGAGCTGACCCAGAGCTGCGCTCACACATGCAG 1250  
 Db 61 CCTGAGCTGTGGAGCTGACCCAGAGAGCTGCGCTCACACATGCAG 16

RESULT 3  
 AM136367/c 412 bp mRNA linear EST 29-OCT-1999  
 LOCUS UI-H-B11-acn-h-02-0-UI.s1 NCI\_CGAP\_Sub3 Homo sapiens cDNA clone  
 DEFINITION IMAGE:2715099 3', mRNA sequence.  
 ACCESSION AM136367  
 VERSION AM136367.1 GI:6140500  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 412)  
 NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of poly A  
 strand cDNA and therefore this may represent a bona fide poly A  
 tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
 NCI\_CGAP clone distribution information can be found through the  
 I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/bnrl/image/image.html The following repetitive  
 elements were found in this cDNA sequence: 200-276,  
 >GC\_rich#low\_complexity  
 Seq primer: M13 Forward  
 POLYA=yes.

FEATURES  
 source Location/Qualifiers

1..412  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2715099"  
 /lab\_host="NCI\_CGAP\_Sub3"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NCI\_CGAP\_Sub3 library is a subtracted library derived from  
 the NCI\_CGAP\_Sub1 library, which is a subtracted library  
 derived from B1. B1 constitutes a mixture of 21  
 normalized or subtracted NCI\_CGAP libraries: NCI\_CGAP\_Co4  
 , NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_Co10,  
 NCI\_CGAP\_Co16, NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid12,  
 NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2,  
 NCI\_CGAP\_Br2, NCI\_CGAP\_Co8, NCI\_CGAP\_CUL1, NCI\_CGAP\_Le12,  
 NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24,  
 NCI\_CGAP\_Lu19, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6,  
 NCI\_CGAP\_Brn25. These 21 libraries were pooled and a  
 single-stranded DNA preparation of the pooled and a  
 single-stranded DNA preparation of the pooled mixture  
 was used as a tracer in a subtractive hybridization with  
 a driver whose composition is detailed below:

NCI\_CGAP\_Kid3 pool 1 LLM 3334-3337, 3682-3683,  
 3798-3803 (IMAGE Clones 1322376-1323911, 1456008-1456775  
 , 1500552-1502855); NCI\_CGAP\_Kid5 pool 1 LLM 3338-3342  
 , 3722-3725, 3776-3778 (IMAGE Clones 1333912-1325831,  
 1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1  
 LLM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991,  
 1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,  
 1469064-1470983, 1475592-1476743); NCI\_CGAP\_Pr22 pool 1  
 LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones  
 985608-986759, 1101192-1101959, 1217928-1220615);  
 NCI\_CGAP\_Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE  
 Clones 1057416-1061255, 1144584-1145351). Subtraction  
 was performed as previously described [Bonaldi, Lennon &  
 Soares (1996): Normalization and Subtraction. Two  
 Approaches to Facilitate Gene Discovery. Genome Research  
 6, 791-806.  
 TAG\_Lib=NCI\_CGAP\_Co10  
 TAG\_Tissue=colon  
 TAG\_Seq=AAACG"  
 BASE COUNT 66 a 132 c 140 g 74 t  
 ORIGIN  
 Query Match 21.0%; Score 371.4; DB 10; Length 412;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-81;  
 Matches 383; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 868 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 927  
 Db 402 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 343  
 QY 928 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 987  
 Db 342 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 283  
 QY 988 CCGGCTGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 1047  
 Db 282 CCGGCTGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 223  
 QY 1048 GAGAGCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 1106  
 Db 222 GAGAGCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 163  
 QY 1107 GCTCTGTACCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 1166  
 Db 162 GCTCTGTACCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGCAAA 103  
 QY 1167 GAAGAGCAAG 1226  
 Db 102 GAAGAGCAAG 43  
 QY 1227 CCAAGACTCGGCTCACACATGCAGT 1251  
 Db 42 CCAAGACTCGGCTCACACATGCAGT 18  
 RESULT 4  
 A1380754/c 376 bp mRNA linear EST 30-MAR-1999  
 LOCUS Lf97905.x1 NCI\_CGAP\_CUL1 Homo sapiens cDNA clone IMAGE:2107256 3',  
 DEFINITION mRNA sequence.  
 ACCESSION A1380754  
 VERSION A1380754.1 GI:4190607  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 376)  
 NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
M.D., Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 479 Std Error: 0.00  
Seq primer: -400P from Glibco.

## FEATURES

source

Location/Qualifiers  
1. 376  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2107256"  
/clone\_lib="NCI-CGAP-CLL1"  
/issue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
was primed with a Not I oligo(dT) primer [5'  
TCTTACCAATCTGAGAGGGAGCGCCGCGATTCTTTTCTTTT  
T 3'] double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified p773 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT

60 a 122 c 133 g 61 t

ORIGIN

Query Match

Best Local Similarity 99.5%; Pred. No. 2e-77; DB 9; Length 376;

Matches 367; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

883 CTCCTCCCGCGCGCTGTTTTCCTGCTGACTTTCAGCGGCGGAAAGCCTGGCCTGCCGC 942  
|||  
376 CTCCTCCCGCGCGCTGTTTTCCTGCTGACTTTCAGCGGCGGAAAGCCTGGCCTGCCGC 317  
|||  
943 CTCACACCGTTCATCTAGAGCAAAATAATGTGAGTGTGCGTGGCCGCTTCCGCTCC 1002  
|||  
316 CTCACACCGTTCATCTAGAGCAAAATAATGTGAGTGTGCGTGGCCGCTTCCGCTCC 257  
|||  
1003 CGGGGACCTGCGGCGGCTGCTGCCAGCCCGGAAACCCGCTGGAGCGCCGTCG 1062  
|||  
256 CGGGGACCTGCGGCGGCTGCTGCCAGCCCGGAAACCCGCTGGAGCGCCGTCG 197  
|||  
1063 CGGGGCGCTTCTCGGAGGACCTACTGCGCACCGCGAAGATT-GGCTCTGTACCGCG 1121  
|||  
196 CGGGGCGCTTCTCGGAGGACCTACTGCGCACCGCGAAGATTGGCTCTGTACCGCG 137  
|||  
1122 GGTCTCTCGGGGCGAGGCGGAGTTCAGGCTTTTCAGGCGCGAGAGAGAGAGAGGAG 1181  
|||  
136 GGTCTCTCGGGGCGAGGCGGAGTTCAGGCTTTTCAGGCGCGAGAGAGAGAGAGGAG 77  
|||  
1182 GATGTCCTCGGGGCGGCGGCGGATTCCTGTGAGCTGTGGAGCTGCACCCAGACTCGCTCA 1241  
|||  
76 GATGTCCTCGGGGCGGCGGCGGATTCCTGTGAGCTGTGGAGCTGCACCCAGACTCGCTCA 17  
|||  
1242 CACATCGAG 1250  
|||  
16 CACATCGAG 8

RESULT 5  
AN207347/c

LOCUS

DEFINITION AM207347 388 bp mRNA linear EST 02-DEC-1999

IMAGE:2723056 3', mRNA sequence.

ACCESSION

AM207347

KEYWORDS

EST.

## SOURCE

ORGANISM

human.

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 388)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrrp/image/image.html The following repetitive  
elements were found in this cDNA sequence: 286-362,  
>GC-rich#Low-complexity  
Seq primer: M13 forward  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers  
1. 388  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2723056"  
/clone\_lib="NCI-CGAP-Sub3"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker. Site.1: Not I; Site.2: Eco RI; The  
NCI-CGAP-Sub3 library is a subtracted library derived from  
the NCI-CGAP-Sub1 library, which is a subtracted library  
derived from BI. BI constitutes a mixture of 21  
normalized or subtracted NCI-CGAP libraries: NCI-CGAP-Co4  
, NCI-CGAP-Pr22, NCI-CGAP-Pr28, NCI-CGAP-Co10,  
NCI-CGAP-Co16, NCI-CGAP-Pr28, NCI-CGAP-Co10,  
NCI-CGAP-Kid3, NCI-CGAP-Kid11, NCI-CGAP-Lym2,  
NCI-CGAP-Br2, NCI-CGAP-Co8, NCI-CGAP-CLL1, NCI-CGAP-Le12,  
NCI-CGAP-Br23, NCI-CGAP-Lu5, NCI-CGAP-Lu24,  
NCI-CGAP-Lu19, NCI-CGAP-GC4, NCI-CGAP-GC6,  
NCI-CGAP-Br25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with  
a driver whose composition is detailed below:  
NCI-CGAP-Kid3 pool 1 LLM 3334-3337, 3682-3683,  
3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775  
, 1500552-1502855); NCI-CGAP-Kid5 pool 1 LLM 3338-3342  
, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831,  
1471368-1472903, 1492104-1493255); NCI-CGAP-Lu5 pool 1  
LLM 33575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991,  
1520904-1522439); NCI-CGAP-GC4 pool 1 LLM 3164-3167,  
3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,  
1469064-1470983, 1475592-1476743); NCI-CGAP-Pr22 pool 1  
LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids  
985608-986759, 1101192-1101959, 1217928-1220615);  
NCI-CGAP-Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE  
Clonoids 1057416-1061255, 1145584-1145351). Subtraction  
was performed as previously described [Bonaldo, Lennon &  
Soares (1996)]: Normalization and Subtraction: Two  
Approaches To Facilitate Gene Discovery. Genome Research  
6, 791-806.  
TAG-LIB=NCI-CGAP-Co10  
TAG-TISSUE=colon  
TAG-SEQ=AAACG.

BASE COUNT

58 a 127 c 132 g 71 t

ORIGIN

Query Match

Best Local Similarity 98.9%; Pred. No. 2.2e-77;

Matches 368; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

968 CAAAAATGTCAGCTGTCGCCGCTCCGCGGAGACTGCGGCGGCTGCCGC 1027



```

|||||
Db 388 CAAAAATGTCAGCTGCTGGCCGCTTGCCGCGGAGACCTGCGGCGGCTGCTGC 329
1028 CAGAGCCCGGACCGCCGCTGAGAGCGCGGCTGCGCCCGGCGCTTCCCGAGGACCTA 1087
328 CAGAGCCCGGACCGCCGCTGAGAGCGCGGCTGCGCCCGGCGCTTCCCGAGGACCTA 269
1088 CTCACACCGGAGAGATT-6GCTCTGTCAGCCCGGCTCTCTCGGGGGCGAGGCGAGGT 1146
268 CTCACACCGGAGAGATTGGGCTCTCTGTCAGCCCGGCTCTCTCGGGGGCGAGGCGAGGT 209
1147 TCAGGCTTTTCAGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
208 TCAGGCTTTTCAGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 149
1207 CTCAGCTGTGGGAGCTGACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1266
148 CTCAGCTGTGGGAGCTGACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 89
1267 TGGGGGGAACGCGAGTCGTCGCGATCCGTCACCCCTGCGCGGAGTGGGGCTTGTGAAC 1326
88 TGGGGGGAACGCGAGTCGTCGCGATCCGTCACCCCTGCGCGGAGTGGGGCTTGTGAAC 29
QY 1327 CCCCCAACCTGA 1338
Db 28 CCCCCAACCTGA 17

RESULT 6
BM695101/c 353 bp mRNA linear EST 28-FEB-2002
LOCUS UI-E-CL1-aes-h-03-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
DEFINITION UI-E-CL1-aes-h-03-0-UI 5', mRNA sequence.
ACCESSION BM695101
VERSION BM695101.1 GI:119008359
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 353)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
COMMENT 97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. 353
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="UI-E-CL1-aes-h-03-0-UI"
/clone_2ib="UI-E-CL1"
/tissue_type="human retina"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CL1 is a normalized cDNA library containing the
following tissue(s): retina. The library was constructed

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BASE COUNT 111 a 88 c 74 g 80 t
ORIGIN
Query Match 19.9%; Score 351.4; DB 14; Length 353;
Best Local Similarity 99.7%; Pred. No. 1,9e-76;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCGCG. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
QY 1323 GAACCCCAACCTGACTGATGGCCAGTGTGTCGCAAAATTGGCAGAGACGAGAGGC 1382
11 CCGCCCGGACCGCCGCTGAGAGCGCGGCTGCGCCCGGCGCTTCCCGAGGACCTA
Db 353 GAGCCCGGACCGCCGCTGAGAGCGCGGCTGCGCCCGGCGCTTCCCGAGGACCTA 294
1383 ACCTCCAAAGTCGCGCAAAATGAATGAGTGGCAGTGAAGCCGGGCTTGTGCTGTG 1442
293 ACCCTCCAAAGTCGCGCAAAATGAATGAGTGGCAGTGAAGCCGGGCTTGTGCTGTG 234
QY 1443 CGTGGCTTCCCGCTCTTCCGCTTTTGTGCTTATGTTATGATTAACCTACTTC 1502
233 CGTGGCTTCCCGCTCTTCCGCTTTTGTGCTTATGTTATGATTAACCTACTTC 174
QY 1503 CTCCTCTGCAAGATTTTGTAGGTTTTCCTTCCCAAGTAGATTCGACAGTCCCG 1562
11 CCGCCCGGACCGCCGCTGAGAGCGCGGCTGCGCCCGGCGCTTCCCGAGGACCTA
Db 173 CTCCTCTGCAAGATTTTGTAGGTTTTCCTTCCCAAGTAGATTCGACAGTCCCG 114
QY 1563 TCAACGGGGTGTGGAGACAGTCATTTTGTGAGAGATCATTTAATTAATGAAT 1622
113 TCAACGGGGTGTGGAGACAGTCATTTTGTGAGAGATCATTTAATTAATGAAT 54
QY 1623 ATTTAATTAAGATTCATTAATGAATTTGCTTCTTTAATGATGA 1675
53 ATTTAATTAAGATTCATTAATGAATTTGCTTCTTTAATGATGA 1
Db 53 ATTTAATTAAGATTCATTAATGAATTTGCTTCTTTAATGATGA 1

RESULT 7
AO229478/c 466 bp DNA linear GSS 26-SEP-1998
LOCUS HS_2021_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2021 COL=16 Row=A, DNA sequence.
ACCESSION AO229478
VERSION AO229478.1 GI:3654707
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,D., Young,D., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT 99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2021 row: A column: 16
Class: BAC ends

```

```

FEATURES                      High quality sequence stop: 466.
Source                        Location/Qualifiers
                                1. 466
                                /organism="Homo sapiens"
                                /db_xref="taxon:9606"
                                /clone_lib="2021 Col=16 Row=A"
                                /sex="male"
                                /note="Organ: sperm; Vector: pBelBAC11; BAC Clones In
                                E-Coli DH10B"
BASE COUNT                    113 a      94 c      111 g      147 t      1 others
ORIGIN

Query Match
Best Local Similarity 90.8%; Pred. No. 1.1e-16;
Matches 118; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGCTACTCAGGAGGCTGAGACAGCAAGAAATCGCTTGACCCGGGAGGAGGAGGTTGCAGTG 60
    |||||||
Db 399 AGCTACTCAGGAGGCTGAGGCGAGAAATCACTTGACCCGAGGAGGTTGCAGTG 340
    |||||

Qy 61 AGCCGAGATCAGCGCCTAGACTCCATCCAGCTGGGCGGAAGAGCAAGACTCCGCTCA 120
    |||||
Db 339 AGCCAGATCAGCGCCTAGCTCCATCCAGCATGGAGAGAGCAAGACTCCGCTCA 280
    |||||

Qy 121 AAAAAAAAAA 130
    |||||||
Db 279 AAAAAAAAAA 270
    |||||||

RESULT 8
AC186502                      680 bp      DNA      linear      GSS 09-JAN-2002
LOCUS                        Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
DEFINITION
AC186502                      sequence.
AC186502                      GSS.
KEYWORDS                      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
SOURCE                        Male BAC Library clone:RP43-060015.T7.
ORGANISM                      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
AUTHORS                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
TITLE                        Totoki,Y., Watanabe,H. and Sakaki,Y.
JOURNAL                      BAC end sequences of Library RPCI-43
REFERENCE
AUTHORS                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
TITLE                        Totoki,Y., Watanabe,H. and Sakaki,Y.
JOURNAL                      Direct Submission
COMMENT                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
                                (E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                                Tel:81-45-503-9111, Fax:81-45-503-9170)
                                Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                end was generated during the R&D process and may have higher chance
                                of clone tracking errors.
                                PRIMERS
                                Sequencing: T7
LIBRARY
Vector                        : pBACe3.6
R.Site 1                      : EcoRI
R.Site 2                      : EcoRI.
Location/Qualifiers
1. 680
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-060015.T7"
/sex="male"
/cell_type="lymphocytes"

```

```

BASE COUNT                    194 a      156 c      163 g      121 t      46 others
ORIGIN

Query Match
Best Local Similarity 87.0%; Pred. No. 2.9e-16;
Matches 120; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 AGTACTCAGGAGGCTGAGACAGCAAGAAATCGCTTGAAACCCGGGAGGAGGTTGCAGTG 60
    |||||||
Db 239 AGTACTCAGGAGGCTGAGAGAGAAATGCTTGAACTGAGAGGAGGTTGCAGTG 298
    |||||||

Qy 61 AGCCGAGATCAGCGCCTAGACTCCATCCAGCTGGGCGGAAGAGCAAGACTCCGCTCA 120
    |||||||
Db 299 AGCCGAGATCAGCGCCTAGCTCCATCCAGCATGGAGAGCAAGACTCCGCTCA 358
    |||||||

Qy 121 AAAAAAAAAATCGTTACA 138
    |||||||
Db 359 AAAAAAAAAAAGAAAAA 376
    |||||||

RESULT 9
AO390169                      418 bp      DNA      linear      GSS 06-MAR-1999
LOCUS                        CITBI-EI-2544A19.TF CITBI-EI Homo sapiens genomic clone 2544A19,
DEFINITION
AO390169                      DNA sequence.
AO390169                      GSS.
KEYWORDS                      AO390169.1 GI:4361192
SOURCE                        human.
ORGANISM                      Homo sapiens
REFERENCE                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS                      Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
                                Venter,J.C.
TITLE                        Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
                                Map Building
JOURNAL                      Unpublished (1997)
COMMENT                      Other_GSSs: CITBI-EI-2544A19.TF
                                Contact: Shaying Zhao, William Nierman, Mark Adams
                                Department of Eukaryotic Genomics
                                The Institute for Genomic Research
                                9712 Medical Center Dr., Rockville, MD 20850
                                Tel: 301 838 0200
                                Fax: 301 838 0208
                                Email: hbe@tigr.org
                                Clones are available from Research Genetics (info@resgen.com). BAC
                                end search page:
                                http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
                                Seq primer: M13-21
                                Class: BAC ends.
FEATURES
Source                        Location/Qualifiers
1. 418
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2544A19"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelBAC11; Site_1: EcoRI; Site_2: EcoRI;
                                Caltech Human BAC Library P"
BASE COUNT                    132 a      109 c      104 g      73 t
ORIGIN

Query Match
Best Local Similarity 86.2%; Pred. No. 6.8e-16;
Matches 119; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 AGTACTCAGGAGGCTGAGACAGCAAGAAATCGCTTGAAACCCGGGAGGAGGTTGCAGTG 60
    |||||
Db 95 AGTCTGAGAGGCTGAGCATGGCAATCACTTGAAACCCGGGAGGAGGTTACAGTG 154
    |||||

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```
0Y 61 AGCCGAGATCAGCGCACTAGATCCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 120
|||||
Db 155 AGCCGAGATCAGCGCACTAGATCCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 214
0Y 121 AAAAAAAAAATCGTTACA 138
|||||
Db 215 AAAAAAAAAAACAACA 232

RESULT 10
BMS09394 469 bp mRNA linear EST 15-FEB-2002
LOCUS 1h17f10.y1 Human Insulinoma Homo sapiens cDNA 5' similar to
DEFINITION SW:AU8.HUMAN P39195 ALU SUBFAMILY SX SEQUENCE CONTAMINATION
WARNING ENTRY. [1] ; mRNA sequence.
ACCESSION BMS09394
VERSION BMS09394
KEYWORDS BMS09394.1 GI:18680537
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hiller,L., Motta,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilll,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 416.
FEATURES
Source location/Qualifiers.
1..469
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Insulinoma"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
XhoI; Site_2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
BASE COUNT 149 a 93 c 94 g 133 t
ORIGIN
Query Match 6.1%; Score 107.2; DB 13; Length 469;
Best Local Similarity 81.6%; Pred. No. 8,6e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
0Y 61 AGCCGAGATCAGCGCACTAGATCCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 120
|||||
Db 345 AGCCGAGATCAGCGCACTAGATCCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 404
0Y 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152
|||||
Db 405 AAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436

RESULT 11
B1468297 516 bp mRNA linear EST 11-MAR-2002
LOCUS 1d87f01.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:5022649
DEFINITION 5', mRNA sequence.
ACCESSION B1468297
VERSION B1468297.1 GI:15284406
KEYWORDS B1468297
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hiller,L., Motta,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilll,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
High quality sequence stop: 457.
FEATURES
Source location/Qualifiers.
1..516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5022649"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
XhoI; Site_2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
BASE COUNT 157 a 103 c 104 g 152 t
ORIGIN
Query Match 6.1%; Score 107.2; DB 13; Length 516;
Best Local Similarity 81.6%; Pred. No. 8,7e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```

OY      61  AGCCGATCATCGCCACTAGACATCCACCTGGGCGGAAGACAGACTCCGTCTCA 120
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      345  AGCCAGGACGACGCGCTGACTCATTCACCTGGGTGACAGACAGACTCATCTCA 404
OY      121  AAAAAAAAAATCGTTACATTATGATGATTT 152
        ||||| || || || || || || || || || || || || || || || || || || ||
DB      405  AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

RESULT 12
LOCUS   BQ270800          529 bp      mRNA      linear      EST 07-MAY-2002
DEFINITION  IK05D06.Y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5779930
ACCESSION BQ270800
VERSION   BQ270800.1 GI:20495866
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 529)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
           Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
           Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
           Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
           'M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,R., Williams,T.,
           Jackson,Y. and Bowers,Y.
           Endocrine Pancreas Consortium
           Unpublished (2000)
           Other-ESTs: IK05D06.x1
           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
           Endocrine Pancreas Consortium
           Harvard University, Howard Hughes Medical Institute
           Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
           MA 02138
           Tel: 617-495-1812
           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           Library was constructed by Dr. J. Ferrer in vivo mass-excised to
           Bluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
           University Genome Sequencing Center for information on obtaining a
           clone please contact: Dr. Hiroshi Inoue (hinoue@lm.wustl.edu)
           Seq primer: -40RP from Gibco
           High quality sequence stop: 428.
           Location/Qualifiers
               1..529
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE: 5779930"
               /clone_lib="Human insulinoma"
               /tissue_type="Human insulinoma"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: pancreas; Vector: pBluescript SK-; Site.1:
               XhoI; Site.2: EcoRI; Constructed with lambda ZapII system
               (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
               pBluescript SK- by Dr. H. Inoue following the Washington
               University protocol
               (http://genome.wustl.edu/est/lambda-protocol.shtml).
               Please contact Hiroshi Inoue, MD/PhD for further
               information on this library (Metabolism Division, Permutt
               Laboratory, Washington University School of Medicine, Box
               8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
               is a Washington University Pancreas EST project library."
BASE COUNT  160 a 107 c 107 g 155 t

Query Match      6.1%; Score 107.2; DB 14; Length 529;
Best Local Similarity 81.6%; Pred. No. 8.7e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY      1  AGCTACTCAGGAGGCTGACACACGAGATCGCTTGAACCCGGAGGAGAGGTTGCAGTG 60

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DB      285  AGCCACTCGGAGGCTTAAATGGAGAAATCGTTGAACCCCTGGAGGAGAGGTTGCAGTG 344
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      61  AGCCGATCATCGCCACTAGACATCCACCTGGGCGGAAGACAGACTCCGTCTCA 120
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      345  AGCCAGGACGACGCGCTGACTCATTCACCTGGGTGACAGACAGACTCATCTCA 404
OY      121  AAAAAAAAAATCGTTACATTATGATGATTT 152
        ||||| || || || || || || || || || || || || || || || || || || ||
DB      405  AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

RESULT 13
LOCUS   BQ267333          556 bp      mRNA      linear      EST 07-MAY-2002
DEFINITION  IK02C03.Y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5779589
ACCESSION BQ267333
VERSION   BQ267333.1 GI:20492398
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 556)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
           Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
           Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
           Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
           'M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,R., Williams,T.,
           Jackson,Y. and Bowers,Y.
           Endocrine Pancreas Consortium
           Unpublished (2000)
           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
           Endocrine Pancreas Consortium
           Harvard University, Howard Hughes Medical Institute
           Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
           MA 02138
           Tel: 617-495-1812
           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           Library was constructed by Dr. J. Ferrer in vivo mass-excised to
           Bluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
           University Genome Sequencing Center for information on obtaining a
           clone please contact: Dr. Hiroshi Inoue (hinoue@lm.wustl.edu)
           Seq primer: -40RP from Gibco
           High quality sequence stop: 428.
           Location/Qualifiers
               1..556
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE: 5779589"
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               /lab_host="DH10B (phage-resistant)"
               /note="Organ: pancreas; Vector: pBluescript SK-; Site.1:
               XhoI; Site.2: EcoRI; Constructed with lambda ZapII system
               (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
               pBluescript SK- by Dr. H. Inoue following the Washington
               University protocol
               (http://genome.wustl.edu/est/lambda-protocol.shtml).
               Please contact Hiroshi Inoue, MD/PhD for further
               information on this library (Metabolism Division, Permutt
               Laboratory, Washington University School of Medicine, Box
               8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
               is a Washington University Pancreas EST project library."
BASE COUNT  167 a 112 c 113 g 164 t

Query Match      6.1%; Score 107.2; DB 14; Length 556;
Best Local Similarity 81.6%; Pred. No. 8.8e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Query Match	6.1%	Score 107.2	DB 14	Length 589
Best Local Similarity	81.6%	Pred. No. 8.8e-16		
Matches 124; Conservative	0	Mismatches 28	Indels 0	Gaps 0

Db 36/ AACCGGATCGGCCCTGCACTCCATCCAGCTGGCAGACAGAGTGAATCCACCTCA 426

Qy 121 AAAAAAAAAATGTTACAT-----TTATGATGATTTACCTCCCTTTTTCACATCA 175

Db 427 AAAAAAAAAAAAAAAAAATTCCTCTTTAACTGATGATACACCCAGTTGATCAGACAA 486

Fri Dec 20 12:19:48 2002

us-09-601-267-1.rst

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[illegible]

Search completed: December 19, 2002, 14:46:57  
Job time : 2153 secs

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